

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-19

Query Match 24.2% Score 16; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAAACGGTAAAA 33
DB 230 CGACAAAACGGTAAAA 245

RESULT 5
US-08-400-256-34
Sequence 34, Application US/08400256
Patent No. 5750497

GENERAL INFORMATION:
APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asger Sloth
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-34

Query Match 24.2% Score 16; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAAACGGTAAAA 33
DB 230 CGACAAAACGGTAAAA 245

RESULT 6

US-08-400-256-43
Sequence 43, Application US/08400256
Patent No. 5750497

GENERAL INFORMATION:
APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asger Sloth
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-43

Query Match 24.2% Score 16; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAAACGGTAAAA 33
DB 230 CGACAAAACGGTAAAA 245

RESULT 7
US-08-975-365-19
Sequence 19, Application US/08975365
Patent No. 6011007

GENERAL INFORMATION:
APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asger Sloth
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2002, 05:43:24 ; Search time 22.2973 Seconds
(without alignments)
727.075 Million col updates/sec

Title: US-09-766-113-2

Perfect score: 66
Sequence: 1 ttaagatcgtatcgttcga.....ccgtctctacgaattcagctg 66

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 48353 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Issued Patents NA:
1: /cgnt2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgnt2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgnt2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgnt2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgnt2_6/ptodata/1/ina/PCrus.COMB.seq.*
6: /cgnt2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	24.2	61	4	US-08-563-524A-10
2	16	24.2	511	1	US-08-400-256-40
3	16	24.2	511	3	US-08-975-365-40
4	16	24.2	523	1	US-08-400-256-19
5	16	24.2	523	1	US-08-400-256-34
6	16	24.2	523	1	US-08-400-256-43
7	16	24.2	523	3	US-08-975-365-19
8	16	24.2	523	3	US-08-975-365-34
9	16	24.2	523	3	US-08-975-365-43
10	16	24.2	535	1	US-08-400-256-46
11	16	24.2	535	3	US-08-975-365-46
12	16	24.2	538	1	US-08-400-256-49
13	16	24.2	538	3	US-08-975-365-49
14	16	24.2	36	1	US-08-136-993-15
15	15	22.7	533	3	US-08-735-545-7
16	15	22.7	533	4	US-09-449-083-7
17	15	22.7	2964	2	US-08-286-819A-18
18	15	22.7	2964	2	US-08-980-357-18
19	15	22.7	3190	2	US-08-286-819A-30
20	15	22.7	3190	3	US-08-980-357-30
21	15	22.7	7004	3	US-09-057-570-3
22	15	22.7	10851	2	US-08-286-819A-16
23	15	22.7	10851	2	US-08-980-357-16
24	14	21.2	24	1	US-08-265-628-10
25	14	21.2	39	1	US-08-459-064B-34
26	14	21.2	39	2	US-08-460-421A-34
27	14	21.2	185	1	US-08-554-369A-1

28	14	21.2	1037	4	US-08-858-207A-149	Sequence 149, App
29	14	21.2	1353	4	US-09-518-657-3	Sequence 3, Appl
30	14	21.2	1598	4	US-09-518-657-6	Sequence 6, Appl
31	14	21.2	2100	1	US-08-332-576-1	Sequence 1, Appl
32	14	21.2	2100	5	PCT-US95-13672-1	Sequence 1, Appl
33	14	21.2	2359	1	US-08-188-582-4	Sequence 4, Appl
34	14	21.2	2359	1	US-08-646-715-4	Sequence 4, Appl
35	14	21.2	6736	3	US-09-057-570-1	Sequence 4, Appl
36	14	21.2	6736	3	US-09-057-570-5	Sequence 5, Appl
37	14	21.2	19332	2	US-08-477-451-25	Sequence 25, Appl
38	13	19.7	18	3	US-09-150-805-3	Sequence 3, Appl
39	13	19.7	18	3	US-09-150-805-13	Sequence 13, Appl
40	13	19.7	18	4	US-08-996-069A-3	Sequence 3, Appl
41	13	19.7	18	4	US-08-996-069A-13	Sequence 13, Appl
42	13	19.7	22	3	US-09-178-089-13	Sequence 13, Appl
43	13	19.7	24	3	US-08-460-173A-25	Sequence 25, Appl
44	13	19.7	24	3	US-08-460-173A-26	Sequence 26, Appl
45	13	19.7	24	3	US-08-464-406A-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-563-524A-10
Sequence 10, Application US/08563524A
Patent No. 6232095
GENERAL INFORMATION:
APPLICANT: Kmiec et al.
TITLE OF INVENTION: Recombinant Helix Modification
TITLE OF INVENTION: Recognition Proteins and Uses Thereof
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/563-524A
FILING DATE: No. 6232095 September 28, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: TUD-1390
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 61
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: NO
US-08-563-524A-10

Query Match 24.2% Score 16; DB 4; Length 61;
Best Local Similarity 100.0% Pred. No. 8.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
50 TCTACGATTAAGCT 65
|||||

db 47 TGTGATGATGATGAT 52

RESULT 2

US-08-400-256-40

Sequence 40, Application US/08400256

Patent No. 5750497

GENERAL INFORMATION:

APPLICANT: Havelund, Sverre

APPLICANT: Halstrom, John

APPLICANT: Jonassen, Ib

APPLICANT: Markussen, Jan

TITLE OF INVENTION: ACYLATED INSULIN

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESS: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/400,256

FILING DATE: 03-MAR-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 3985,220-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 511 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-400-256-40

Query Match 24.2% Score 16; DB 1; Length 511;

Host Local Similarity 100.0%; Pred. No. 6.4;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

db 47 TGTGATGATGATGAT 52

db 227 GCACAAACCGTAA 242

RESULT 3

US-08-975-365-40

Sequence 40, Application US/08975365

Patent No. 6011007

GENERAL INFORMATION:

APPLICANT: Havelund, Sverre

APPLICANT: Halstrom, John

APPLICANT: Jonassen, Ib

APPLICANT: Markussen, Jan

TITLE OF INVENTION: ACYLATED INSULIN

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESS: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/975,365

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/400,256

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 3985,220-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 511 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-975-365-40

Query Match 24.2% Score 16; DB 3; Length 511;

Host Local Similarity 100.0%; Pred. No. 6.4;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

db 47 TGTGATGATGATGAT 52

db 227 GCACAAACCGTAA 242

RESULT 4

US-08-400-256-19

Sequence 19, Application US/08400256

Patent No. 5750497

GENERAL INFORMATION:

APPLICANT: Havelund, Sverre

APPLICANT: Halstrom, John

APPLICANT: Jonassen, Ib

APPLICANT: Markussen, Jan

TITLE OF INVENTION: ACYLATED INSULIN

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESS: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/400,256

FILING DATE: 03-MAR-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 3985,220-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-19

Query Match 24.2% Score 16; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACCGTAAAA 33
|||||
DB 230 CGACAAACCGTAAAA 245

RESULT 5
US-08-400-256-34
Sequence 34, Application US/08400256
Patent No. 5750497

GENERAL INFORMATION:

APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asger Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-34

Query Match 24.2% Score 16; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACCGTAAAA 33
|||||
DB 240 CGACAAACCGTAAAA 245

RESULT 6

US-08-400-256-43
Sequence 43, Application US/08400256
Patent No. 5750497

GENERAL INFORMATION:
APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asger Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-43

Query Match 24.2% Score 16; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACCGTAAAA 33
|||||
DB 230 CGACAAACCGTAAAA 245

RESULT 7

US-08-975-365-19
Sequence 19, Application US/08975365
Patent No. 6011007

GENERAL INFORMATION:
APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asger Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,365
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

RESULT 10
US-08-400-256-46
Sequence 46, Application US/08400256
Patent No. 5750497
GENERAL INFORMATION:
APPLICANT: Havelund, Syvend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400.256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-46
Query Match 24.2%; Score 16; DB 1; Length 535;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGGTAAAA 33
|||||
DB 227 CGACAAACGGTAAAA 242

RESULT 11
US-08-975-365-46
Sequence 46, Application US/08975365
Patent No. 6011007
GENERAL INFORMATION:
APPLICANT: Havelund, Syvend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asger Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975.365
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400.256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-975-365-46
Query Match 24.2%; Score 16; DB 3; Length 535;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGGTAAAA 33
|||||
DB 227 CGACAAACGGTAAAA 242

RESULT 12
US-08-400-256-49
Sequence 49, Application US/08400256
Patent No. 5750497
GENERAL INFORMATION:
APPLICANT: Havelund, Syvend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asger Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400.256
FILING DATE: 03-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ. ID NO: 49:

SEQUENCE CHARACTERISTICS:
LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-400-256-49

Query Match 24.28; Score 16; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGGTAAAA 33
DB 227 CGACAAACGGTAAAA 242

RESULT 13

US-08-975-465-49
Sequence 49, Application US/08975365
PATENT No. 6011007
GENERAL INFORMATION:
APPLICANT: Haveland, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Audestsen, Asger Sten
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACTIVATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 60110070 No. 6011007disk of No. 6011007Lb America, Inc.
STREET: 405 Lexington Avenue, 64th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
TELEPHONE: 202-293-7860
TELEFAX: 202-293-7860
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,465
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 04-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambilis, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985,220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-975-465-49

Query Match 24.28; Score 16; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGGTAAAA 33
DB 227 CGACAAACGGTAAAA 242

RESULT 14

US-08-136-993-15/c
Sequence 15, Application US/08136993
PATENT No. 542025
GENERAL INFORMATION:
APPLICANT: Takagi, Hiroshi
APPLICANT: Araioka, Shiro
APPLICANT: Matsui, Hiroshi
APPLICANT: Washizu, Kiyoa
APPLICANT: Ando, Keiichi
APPLICANT: Kotaka, Satoshi
TITLE OF INVENTION: Recombinant transglutaminase
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Squibb, Mon, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
STATE: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,993
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/777,447
FILING DATE:
APPLICATION NUMBER: JP 2-282506
FILING DATE: 19-OCT-1990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-293-7060
TELEFAX: 202-293-7860
TELEX: 6491104
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-136-993-15

Query Match 22.78; Score 15; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCGATCGG 15
DB 16 TGAGATCGATCGG 2

RESULT 15

US-08-735-545-7
Sequence 7, Application US/08735545
PATENT No. 6025131
GENERAL INFORMATION:
APPLICANT: Van Dyk, Tina K.
APPLICANT: Lakossa, Robert Alan
TITLE OF INVENTION: A Facile Method for
IDENTIFYING REGULATED
TITLE OF INVENTION: Identifying Regulated
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: E. T. DU PONT DE NEMOURS
ADDRESSER: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE

COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,545
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: dpd2087 upper
US-08-735-545-7

Query Match 22.7%; Score 15; DB 3; Length 533;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 AAACGGTAAAAAG 36
|||||
DB 72 AAACGGTAAAAAG 86

RESULT 16
US-09-449-083-7
Sequence 7, Application US/09449083
Patent No. 6194159
GENERAL INFORMATION:
APPLICANT: Van Dyk, Tina K.
APPLICANT: Larossa, Robert Alan
TITLE OF INVENTION: A Facile Method for
TITLE OF INVENTION: Identifying Regulated
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/449,083
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A.
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: dpd2087 upper
US-09-449-083-7

Query Match 22.7%; Score 15; DB 4; Length 533;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 AAACGGTAAAAAG 36
|||||
DB 72 AAACGGTAAAAAG 86

RESULT 17
US-08-286-819A-18
Sequence 18, Application US/08286819A
Patent No. 5871910
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPROTEINS, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NITROGEN-SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.-C.
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2964 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2964
US-08-286-819A-18

Query Match 22.7% Score 15; DB 2; Length 2964;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACAAAACGCTAAAAA 34
DB 966 ACAAAACGCTAAAAA 980

RESULT 18
US-08-980-357-18
Sequence 18, Application US/08980357
Patent No. 6014508
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALIN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPETIDES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 6014508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2964 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2964
US-08-980-357-18

Query Match 22.7% Score 15; DB 3; Length 2964;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACAAAACGCTAAAAA 34
DB 966 ACAAAACGCTAAAAA 980

RESULT 19
US-08-286-819A-30
Sequence 30, Application US/08286819A
Patent No. 5871910
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALIN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPETIDES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 3190 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-286-819A-30

Query Match 22.7% Score 15; DB 2; Length 3190;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 20 ACAAACGGTAAAA 34
|||||
DB 1115 ACAAACGGTAAAA 1129

RESULT 20
US-08-980-357-30
Sequence 30, Application US/08980357
Patent No. 6013508
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GINGIPEPTIDES, IN PARTICULAR
TITLE OF INVENTION: IN GRAP-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000

TELEPHONE: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 3190 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-980-357-30

Query Match 22.7% Score 15; DB 3; Length 3190;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 20 ACAAACGGTAAAA 34
|||||
DB 1115 ACAAACGGTAAAA 1129

RESULT 21
US-09-057-570-3/C
Sequence 3, Application US/09057570
Patent No. 6013266
GENERAL INFORMATION:
APPLICANT: Sectors, Round P.A.M.
APPLICANT: Frey, Joachim
TITLE OF INVENTION: Live attenuated Actinobacillus
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 6013266el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EP0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,570
FILING DATE: 09-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Gornley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 948-7400
TELEFAX: (301) 948-9751
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7004 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
STRAIN: HV114 (serotype 3 field strain)
IMMEDIATE SOURCE:
CLONE: FROKS
FEATURE:
NAME/KEY: CDS
LOCATION: 1566..5714
OTHER INFORMATION: /codon_start=1566
OTHER INFORMATION: /function="rtx-toxin"
OTHER INFORMATION: /product="ApvIV_var3"
OTHER INFORMATION: /gene="apvIV_var3"
OTHER INFORMATION: /number=1

US-09-057 570-4

Query Match 22.7%; Score 15; DB 3; Length 7004;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TAAAAAGCTGAC 43
|||||
ID 542 TAAAAAGCTGAC 528

RESULT 22

US-08-286 819A-16/c
Sequence 16, Application US/08286819A
Patent No. 5871910
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DOKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: CORRAVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: ORLON, SPIVAK, MCCLELLAND, WATER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ORLON, NO. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/BOOKLET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-4000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 10851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08 286-819A-16

Query Match 22.7%; Score 15; DB 2; Length 10851;

Best Local Similarity 100.0%; Pred. No. 14;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACAAAACGCTAAAA 34
|||||
ID 2076 ACAAAACGCTAAAA 2062

RESULT 23

US-08-980-357-16/c
Sequence 16, Application US/08980357
Patent No. 6013508
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DOKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: CORRAVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: ORLON, SPIVAK, MCCLELLAND, WATER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ORLON, NO. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/BOOKLET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 10851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08 980-357-16

Query Match 22.7%; Score 15; DB 3; Length 10851;

Host Local Similarity 100.0%; Pred. No. 14;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACMAAGCTAATAA 34
|||||

Db 2076 ACMAAGCTAATAA 2062

RESULT 24

US-08-265-628-10/c

Sequence 10, Application US/08265628

Patent No. 5821094

GENERAL INFORMATION:

APPLICANT: Rothstein, Steven J.

APPLICANT: Goring, Daphne

TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A

TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 W. Madison St. Suite 3400

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/265,628

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/959,945

FILING DATE:

APPLICATION NUMBER: US 07/847,564

FILING DATE: 03-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Pochopion Ph.D., Donald J.

REGISTRATION NUMBER: 32,167

TELEPHONE: 312-707-8889

TELEFAX: 312-707-9155

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..24

US-08-265-628-10

Query Match 21.2%; Score 14; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1,16+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGATCTGATCG 15
|||||

Db 15 GAGATCTGATCG 2

RESULT 25

US-08-459-064B-34/c

Sequence 34, Application US/08459064B

Patent No. 5747452

GENERAL INFORMATION:

APPLICANT: ROUSLARTI, ERKKI I.

APPLICANT: MORLA, ALEX

TITLE OF INVENTION: A METHOD OF MODULATING TUMOR CELL MIGRATION

TITLE OF INVENTION: USING FIBRONECTIN TYPE III PEPTIDES

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSSEE: CAMPBELL & FLORES LLP

STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700

CITY: SAN DIEGO

STATE: CALIFORNIA

COUNTRY: UNITED STATES

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,064B

FILING DATE: 01-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/829,462

FILING DATE: 31-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/021,626

FILING DATE: 16-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/340,812

FILING DATE: 17-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, CATHERYN A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-1A 1543

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-535-9001

TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: circular

FEATURE:

NAME/KEY: CDS

LOCATION: 1..37

US-08-459-064B-34

Query Match 21.2%; Score 14; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 16+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGCTCGATCG 14
|||||

Db 20 TGAGCTCGATCG 7

RESULT 26

US-08-460-421A-34/c

Sequence 34, Application US/08460421A

Patent No. 5837813

GENERAL INFORMATION:

APPLICANT: ROUSLARTI, ERKKI I.

APPLICANT: MORLA, ALEX

TITLE OF INVENTION: FIBRONECTIN BINDING SITES AND METHODS OF

TITLE OF INVENTION: MODULATING FIBRONECTIN EXTRACELLULAR MATRIX ASSEMBLY

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSSEE: CAMPBELL & FLORES LLP

STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700

CITY: SAN DIEGO

STATE: CALIFORNIA

COUNTRY: UNITED STATES

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patient In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,421A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,462
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,626
FILING DATE: 16-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,812
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1A 1542
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
FEATURE:
NAME/KEY: CDS
LOCATION: 1..17
US-08-460 421A-14

Query Match 21.2%; Score 14; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1002;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGTCGATCGCT 14
DB 20 TCAGTCGATCGCT 7

RESULT 27
US-08-554-369A-1
Sequence 1, Application US/0854369A
Patent No. 5824519
GENERAL INFORMATION:
APPLICANT: MORRIS, JAMES S.
APPLICANT: CLARKSON, GARY A.
TITLE OF INVENTION: TISSUE SPECIFIC AND TARGET RNA SPECIFIC
TITLE OF INVENTION: KIBOZYMS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 40403
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patient In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,369A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 19070.0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-08-554-369A-1

Query Match 21.2%; Score 14; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGATCTGATCGCT 16
DB 112 AGATCTGATCGCT 125

RESULT 28
US-08-858-207A-149
Sequence 149, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stedolas, Robert
TITLE OF INVENTION: No. 6348328el compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmtLinkline Beecham Corporation
STREET: 709 Swedland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R.
REGISTRATION NUMBER: 48,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-858-207A-149

Query Match 21.2%; Score 14; DB 4; Length 1037;
Best Local Similarity 100.0%; Pred. No. 63;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 CCTGACATTCAGC 64
|||||

DB 595 CCTGACATTCAGC 608

RESULT 29
US-09-518-657-3
Sequence 3, Application US/09518657
Patent No. 6335188
GENERAL INFORMATION:
APPLICANT: Schardl, Christopher L.
APPLICANT: Wang, Jinghong
TITLE OF INVENTION: Endophyte Ectot Alkaloid Synthetic Compounds, Compounds
TITLE OF INVENTION: Which Encode Therefor and Related Methods
FILE REFERENCE: P-1060
CURRENT APPLICATION NUMBER: US/09/518,657
CURRENT FILING DATE: 2000-03-03
EARLIER APPLICATION NUMBER: 60/125,490
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Neotyphodium coenophialium
US-09-518-657-3

Query Match
Best Local Similarity 100.0%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATCTGATCGTTC 18
|||||

DB 438 ATCTGATCGTTC 351

RESULT 30
US-09-518-657-6
Sequence 6, Application US/09518657
Patent No. 6335188
GENERAL INFORMATION:
APPLICANT: Schardl, Christopher L.
APPLICANT: Wang, Jinghong
TITLE OF INVENTION: Endophyte Ectot Alkaloid Synthetic Compounds, Compounds
TITLE OF INVENTION: Which Encode Therefor and Related Methods
FILE REFERENCE: P-1060
CURRENT APPLICATION NUMBER: US/09/518,657
CURRENT FILING DATE: 2000-03-03
EARLIER APPLICATION NUMBER: 60/125,490
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 6
LENGTH: 1598
TYPE: DNA
ORGANISM: Neotyphodium coenophialium
US-09-518-657-6

Query Match
Best Local Similarity 100.0%; Pred. No. 59;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATCTGATCGTTC 18
|||||

DB 362 ATCTGATCGTTC 375

RESULT 41
US-08-312-576-1
Sequence 1, Application US/08312576
Patent No. 5756105

GENERAL INFORMATION:
APPLICANT: Welser, Jeffrey M.
TITLE OF INVENTION: Vaccines for Haemophilis Influenza
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and No. 5756105r1s
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,576
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/CHECK NUMBER: CH-536
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3434

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1553..2005
FEATURE:
NAME/KEY: CDS
LOCATION: 209..1492

US-08-332-576-1
Query Match
Best Local Similarity 100.0%; Pred. No. 57;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AAAAAGCGGTACA 43
|||||

DB 1025 AAAAAGCGGTACA 1038

RESULT 32
PCT-US95-13672-1
Sequence 1, Application PC/TUS9513672
GENERAL INFORMATION:
APPLICANT: Welser, Jeffrey M.
TITLE OF INVENTION: Vaccines for Haemophilis Influenza
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13672

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 49..2160
US-08-646-715-4

Query Match 21.2%: Score 14; DB 1; Length 2356;
Best Local Similarity 100.0%: Pred. No. 56;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GATCCCTTGACA 22
Db 1875 GCATCCTTGACA 1862

RESULT 35
US-09-057-570-1/c
Sequence 1, Application US/09057570
Patent No. 6013266
GENERAL INFORMATION:
APPLICANT: Segers, Ruud P.A.M.
APPLICANT: Frey, Joachim
TITLE OF INVENTION: Live attenuated Actinobacillus
TITLE OF INVENTION: pleuropneumoniae
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Akzo No. 6013266el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,570
FILING DATE: 09-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 948-7400
TELEFAX: (301) 948-9751
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6736 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
STRAIN: 4074 (serotype 1 reference strain)
IMMEDIATE SOURCE:
CLONE: PROK7
FEATURE:
NAME/KEY: CDS
LOCATION: 1576..6549
OTHER INFORMATION: /codon_start= 1576
OTHER INFORMATION: /function= "RTX-toxin"
OTHER INFORMATION: /product= "ApXIV_vari"
OTHER INFORMATION: /gene= "ApXIV_vari"
OTHER INFORMATION: /number= 1
US-09-057-570-1

Query Match 21.2%: Score 14; DB 3; Length 6736;
Best Local Similarity 100.0%: Pred. No. 48;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TAAAGGCGTAG 42

Db 531 TAAAGGCGTAG 518

RESULT 36
US-09-057-570-5/c
Sequence 5, Application US/09057570
Patent No. 6013266
GENERAL INFORMATION:
APPLICANT: Segers, Ruud P.A.M.
APPLICANT: Frey, Joachim
TITLE OF INVENTION: Live attenuated Actinobacillus
TITLE OF INVENTION: pleuropneumoniae
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Akzo No. 6013266el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,570
FILING DATE: 09-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 948-7400
TELEFAX: (301) 948-9751
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6736 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
STRAIN: 4074 (serotype 1 reference strain)
IMMEDIATE SOURCE:
CLONE: PROK7
FEATURE:
NAME/KEY: CDS
LOCATION: 1132..6549
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start= 1132
OTHER INFORMATION: /function= "RTX toxin"
OTHER INFORMATION: /product= "ApXIV"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ApXIV_v1"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..453
OTHER INFORMATION: /partial
OTHER INFORMATION: /product= "Met-G"
OTHER INFORMATION: /gene= "mrp"
OTHER INFORMATION: /standard_name= "mrp"
OTHER INFORMATION: /label= mrp
FEATURE:
NAME/KEY: -10_signal
LOCATION: 617..623
OTHER INFORMATION: /standard_name= "-10"
OTHER INFORMATION: /label= -10_s
FEATURE:
NAME/KEY: -35_signal

LOCATION: 594..599
 OTHER INFORMATION: /standard name: *-35_s"
 OTHER INFORMATION: /label: -35_s"
 FEATURE:
 NAME/KEY: promoter
 LOCATION: 454..1131
 OTHER INFORMATION: /function: "Promoter"
 OTHER INFORMATION: /standard name: "promoter Apv1v"
 OTHER INFORMATION: /label: promoter
 US-09-057-570-5

Query Match 21.2% Score 14; DB 3; Length 6716;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TAAAAAGCGGTAG 42
 |||||
 DB 541 TAAAAAGCGGTAG 518

RESULT 47

US-08-477-451-25
 Sequence 25, Application US/08477451
 Patent No. 5928865
 GENERAL INFORMATION:
 APPLICANT: Covacel, Autodello
 TITLE OF INVENTION: Heptobacter pylori CagI Region
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHIRON Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608-2916
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,451
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Reising, Barbara G.
 REGISTRATION NUMBER: 34,114
 REFERENCE/DOCKET NUMBER: 0435,002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-601-2708
 TELEFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19932 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-477-451-25

Query Match 21.2% Score 14; DB 2; Length 19932;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TAAAAAGCGGTAG 42
 |||||
 DB 829 TAAAAAGCGGTAG 842

RESULT 48
 US-09-150-805-1
 Sequence 3, Application US/09150805
 Patent No. 6140080

GENERAL INFORMATION:
 APPLICANT: Bruce, Wesley
 APPLICANT: Lu, Guihua
 TITLE OF INVENTION: PROMOTER ELEMENTS CONFERRING
 TITLE OF INVENTION: ROOT-PREFERRED GENE EXPRESSION
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
 STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
 STREET: Box 1000
 CITY: Johnston
 STATE: Iowa
 COUNTRY: USA
 ZIP: 50131

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/150,805
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,069
 FILING DATE: 22-DEC-1997
 APPLICATION NUMBER: US 08/649,172
 FILING DATE: 17-MAY-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Yates, Michael E.
 REGISTRATION NUMBER: 36,063
 REFERENCE/DOCKET NUMBER: 46,063
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (515) 248-4800
 TELEFAX: (515) 248-4844
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "oligonucleotide"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..18
 OTHER INFORMATION: /product = "N7911"

US-09-150-805-3

Query Match 19.7% Score 13; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3,76+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATCGATCGGT 17
 |||||
 DB 5 ATCGATCGGT 17

RESULT 39
 US-09-150-805-13
 Sequence 13, Application US/09150805
 Patent No. 6140080

GENERAL INFORMATION:
 APPLICANT: Bruce, Wesley
 APPLICANT: Lu, Guihua
 TITLE OF INVENTION: PROMOTER ELEMENTS CONFERRING
 TITLE OF INVENTION: ROOT-PREFERRED GENE EXPRESSION
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
 STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
 STREET: Box 1000
 CITY: Johnston

STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,805
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/996,069
FILING DATE: 22-DEC-1997
APPLICATION NUMBER: US 08/649,172
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.
REGISTRATION NUMBER: 36,063
REFERENCE/DOCKET NUMBER: 0465R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-150-805-13

Query Match 19.7% Score 13; DB 3; Length 18;
Best local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATCTGATCGGTT 17
|||||
DB 5 ATCTGATCGGTT 17

RESULT 40
US-08-996-069A-1
Sequence 3, Application US/08996069A
Patent No. 6228645
GENERAL INFORMATION:
APPLICANT: Bruce, Wesley
TITLE OF INVENTION: PROMOTER ELEMENTS CONFERRING
TITLE OF INVENTION: ROOT-PREFERRED GENE EXPRESSION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,069A
FILING DATE: 22-DEC-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/649,172
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:

NAME: Yates, Michael E.
REGISTRATION NUMBER: 36,063
REFERENCE/DOCKET NUMBER: 0465R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
FEATURE: misc_feature
NAME/KEY: misc
LOCATION: 1..18
OTHER INFORMATION: /product= "N7913"
US-08-996-069A-3

Query Match 19.7% Score 13; DB 4; Length 18;
Best local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATCTGATCGGTT 17
|||||
DB 5 ATCTGATCGGTT 17

RESULT 41
US-08-996-069A-13
Sequence 13, Application US/08996069A
Patent No. 6228645
GENERAL INFORMATION:
APPLICANT: Bruce, Wesley
TITLE OF INVENTION: PROMOTER ELEMENTS CONFERRING
TITLE OF INVENTION: ROOT-PREFERRED GENE EXPRESSION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,069A
FILING DATE: 22-DEC-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/649,172
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.
REGISTRATION NUMBER: 36,063
REFERENCE/DOCKET NUMBER: 0465R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-996-069A-14

Query Match 19.7% Score 13; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3,6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACATCTGATCCCT 17
DB 5 ACATCTGATCCCT 17

RESULT 42

US-09-178-089-13/c

Sequence 13; Application US/09178089
Patent No. 6077992

GENERAL INFORMATION:
APPLICANT: YADAV, NARENDRA S.
TITLE OF INVENTION: BINARY VIRAL EXPRESSION SYSTEM IN PLANTS
FILE REFERENCE: CI-1127
CURRENT APPLICATION NUMBER: US/09/178,089
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: OCTOBER 24, 1997
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 13
LENGTH: 22
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism-primers
US-09-178-089-13

Query Match 19.7% Score 13; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 3,6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GATCTGATCCCT 16
DB 14 GATCTGATCCCT 2

RESULT 43

US-08-480-173A-25

Sequence 25; Application US/08480173A
Patent No. 6072049

GENERAL INFORMATION:
APPLICANT: Thomas, Haas A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Wiles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED100305D4
TELEPHONE: 612-344-8991
TELEFAX: 612-344-8991

INFORMATION FOR SEQ ID NO: 25;

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..4

OTHER INFORMATION: /note= "Nucleotides 1-4 form a

OTHER INFORMATION: single-stranded "sticky end"

FEATURE:

NAME/KEY: misc_feature

LOCATION: 5..24

OTHER INFORMATION: /note= "Adapter sequence results

OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-2

OTHER INFORMATION: SEQ ID NO: 26"

US-08-480-173A-25

Query Match 19.7% Score 13; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 3,5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACATCTGATCCG 15
DB 6 ACATCTGATCCG 18

RESULT 44

US-08-480-173A-26/c

Sequence 26; Application US/08480173A
Patent No. 6072049

GENERAL INFORMATION:
APPLICANT: Thomas, Haas A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Wiles, P.A.
STREET: 80 S. 8th Street, Suite 1902
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Popovich, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED100305D4
TELEPHONE: 612-344-8991
TELEFAX: 612-344-8991
INFORMATION FOR SEQ ID NO: 26;
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4
OTHER INFORMATION: /note= "Nucleotides 1-4 form a
OTHER INFORMATION: single-stranded "sticky end"

NAME/KEY: misc_feature
 LOCATION: 5..24 /note= "Adapter sequence results
 OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24
 OTHER INFORMATION: SEQ ID NO: 25"
 US-08-480-173A-26

Query Match 19.7%; Score 13; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGATCTGATCG 15
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 DB 23 AGATCTGATCG 11

RESULT 45

US-08-484-408A-25
 : Sequence 25; Application US/08484408A
 : Patent No. 6117653
 : GENERAL INFORMATION:
 : APPLICANT: Thoma, Hans A
 : TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
 : NUMBER OF SEQUENCES: 56
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Popovich & Miles, P.A.
 : STREET: 80 S. 8th Street, Suite 1902
 : CITY: Minneapolis
 : STATE: MN
 : COUNTRY: USA
 : ZIP: 55402
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/484,408A
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Popovich, Thomas E
 : REGISTRATION NUMBER: 30,099
 : REFERENCE/DOCKET NUMBER: MED100305D4
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 612-334-8991
 : TELEFAX: 612-334-8994
 : INFORMATION FOR SEQ ID NO: 25:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 24 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (synthetic)
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: 1..4
 : OTHER INFORMATION: /note= "Nucleotides 1-4 form a
 : OTHER INFORMATION: single-stranded "sticky end"
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: 5..24
 : OTHER INFORMATION: /note= "Adapter sequence results
 : OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-24
 : OTHER INFORMATION: SEQ ID NO: 26"
 : US-08-484-408A-25

DB 6 AGATCTGATCG 18
 Search completed: November 5, 2002, 08:26:11
 Job time : 37.2973 secs

Query Match 19.7%; Score 13; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGATCTGATCG 15
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REFERENCE 1 (bases 1 to 3012)
AUTHORS Kimmerly,W.J.
TITLE Staphylococcus epidermidis nucleic acids and proteins
JOURNAL Patent: WO 0134809-A 3924 17-MAY-2001;
        GLAXO GROUP LIMITED (GB)
FEATURES
    source
        1. 3032
            /organism="Synthetic Construct"
            /db_xref="taxon:32630"
            /note="synthetic nucleic acid sequence"
BASE COUNT 939 a 600 c 422 g 1071 t
ORIGIN
Query Match 24.2% Score 16: DB 6; Length 3032;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 29 TAAAAAGCGGTAGAT 44
      |||||||
Db 3026 TAAAAAGCGGTAGAT 3011

RESULT 44
AF269294 3246 bp DNA linear BCT 06-DXC-2001
LOCUS Staphylococcus epidermidis strain SRI clone step.1000c01 genomic
sequence.
ACCESSION AF269294
VERSION AF269294.1 GI:9664615
KEYWORDS
SOURCE
ORGANISM
    Staphylococcus epidermidis.
    Staphylococcus epidermidis.
    Bacteria: Firmicutes; Bacillus/Clostridium group;
    Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 3246)
    Kimmerly,W.J., Taylor,J.D., Nelson,A.J., Godlevski,M.M.,
    Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
    Listebbee,S., Ashanti,C., Altschuller,G., Mamo,L., Shepherd,N.S.,
    Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
    Furdos,P.J.
    Transposon-mediated sequencing of the Staphylococcus epidermidis
    genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3246)
    Taylor,J.D., Kimmerly,W.J., Nelson,A.J., Godlevski,M.M.,
    Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
    Listebbee,S., Ashanti,C., Altschuller,G., Mamo,L., Shepherd,N.S.,
    Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
    Furdos,P.J.
    Direct Submission
JOURNAL Submitted (19 MAY 2000) Departments of Genomic Sciences and
    Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
    Drive, Research Triangle Park, North Carolina 27709-3398, USA
FEATURES
    source
        1. 3246
            /organism="Staphylococcus epidermidis"
            /strain="SKI"
            /db_xref="taxon:1282"
            /clone="step.1000c01"
BASE COUNT 1091 a 533 c 536 g 1086 t
ORIGIN
Query Match 24.2% Score 16: DB 1; Length 3246;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 29 TAAAAAGCGGTAGAT 44
      |||||||
Db 2668 TAAAAAGCGGTAGAT 2683

RESULT 45
AX144614

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LOCUS AX144614 3246 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 3336 from Patent W00134809.
ACCESSION AX144614
VERSION AX144614.1 GI:14283179
KEYWORDS
SOURCE
    synthetic construct.
    synthetic construct.
    artificial sequence.
REFERENCE 1 (bases 1 to 3246)
AUTHORS Kimmerly,W.J.
TITLE Staphylococcus epidermidis nucleic acids and proteins
JOURNAL Patent: WO 0134809-A 3336 17-MAY-2001;
        GLAXO GROUP LIMITED (GB)
FEATURES
    source
        1. 3246
            /organism="Synthetic Construct"
            /db_xref="taxon:32630"
            /note="synthetic nucleic acid sequence"
BASE COUNT 1091 a 533 c 536 g 1086 t
ORIGIN
Query Match 24.2% Score 16: DB 6; Length 3246;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 29 TAAAAAGCGGTAGAT 44
      |||||||
Db 2668 TAAAAAGCGGTAGAT 2683

Search completed: November 5, 2002, 09:20:43
Job time : 504.822 secs

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SOURCE Schizosaccharomyces pombe DNA.
ORGANISM Schizosaccharomyces pombe.
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycotales; Schizosaccharomycetaceae;
Schizosaccharomycos.
REFERENCE
1 (sites)
Osaka, F., Seno, H., Seno, T. and Yamao, F.
TITLE A ubiquitin-conjugating enzyme in fission yeast that is essential
for the onset of anaphase in mitosis
Mol. Cell. Biol. 17 (6), 388-397 (1997)
JOURNAL
9729689
2 (sites)
Osaka, F., Seno, H., Seno, T. and Yamao, F.
REFERENCE
TITLE An ubiquitin-conjugating enzyme in the fission yeast, essential for
onset of anaphase in mitosis
Unpublished (1996)
JOURNAL
3 (bases 1 to 1613)
Osaka, F.
REFERENCE
TITLE Direct Submission
Submitted (23-MAY-1996) Fumio Osaka, National Institute of
Genetics, 111 Yata, Mishima, Shizuoka 411, Japan
(Tel.:0559-81-6748)
FEATURES
SOURCE
1..1613
location/Qualifiers
/organism="Schizosaccharomyces pombe"
/db_xref="taxon:4896"
/gene="ubp4"
/complement(1..35)
/gene="chk1"
/complement(1..35)
/gene="chk1"
/codon_start=1
/product="protein kinase"
/protein_id="BAA20374.1"
/db_xref="GI:2190254"
/translation="MAQKIDNPYH"
c318..412
/gene="ubp4"
/number=1
join(318..412,461..488,539..628,779..1014,1065..1146)
/gene="ubp4"
join(318..412,461..488,539..628,779..1014,1065..1146)
/gene="ubp4"
/note="ubiquitin-conjugating enzyme"
/codon_start=1
/product="ubp4"
/protein_id="BAA20375.1"
/db_xref="GI:2190255"
/translation="MDSDMDNDNDPTNSKSSSGAMVADGSHVTKRLRSLMSLMSN
TGLTSAEPDSDNLLIMACTITGSDPYRDLKKLSMSPPANPYSPPTITSSM
HPNVDMSGNCIDILKKMSAVNYQTILSLQSLDEPNASFLNQAALMSKPI
EYKRLIMQRTKIDET"
413..460
/gene="ubp4"
/number=1
461..488
/gene="ubp4"
/number=2
489..538
/gene="ubp4"
/number=2
539..628
/gene="ubp4"
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629..778
/gene="ubp4"
/number=4
779..1014
/gene="ubp4"
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1015..1064
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/number=4
1065..1146

BASE COUNT 495 a 265 c 263 g 549 t 1 others
ORIGIN
Query Match 24.2%; Score 16; DB 8; Length 1613;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GY 20 ACAAACCGTAAAAA 45
DB 405 ACAAACCGTAAAAA 420
RESULT 42
AF269884/c
LOCUS
DEFINITION
Staphylococcus epidermidis strain SK1 clone step.1028c03 genomic
sequence.
ACCESSION
AF269884
VERSION
AF269884.1 GI:9623784
KEYWORDS
SOURCE
ORGANISM
Staphylococcus epidermidis.
Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE
1 (bases 1 to 3032)
Kimmerly, W.J., Taylor, J. David., Nelson, A.J., Gollivski, M.M.,
Rubino, M.A., Nelson, P.J., Rivers, P.R., Tortorella-Miller, J.,
Listebeebe, S., Ashanti, C., Altshuler, G., Mamola, S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
TITLE Transposon-mediated sequencing of the Staphylococcus epidermidis
genome
Unpublished
2 (bases 1 to 3032)
Taylor, J. David., Kimmerly, W.J., Nelson, A.J., Gollivski, M.M.,
Rubino, M.A., Nelson, P.J., Rivers, P.R., Tortorella-Miller, J.,
Listebeebe, S., Ashanti, C., Altshuler, G., Mamola, S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
JOURNAL
2 (bases 1 to 3032)
Taylor, J. David., Kimmerly, W.J., Nelson, A.J., Gollivski, M.M.,
Rubino, M.A., Nelson, P.J., Rivers, P.R., Tortorella-Miller, J.,
Listebeebe, S., Ashanti, C., Altshuler, G., Mamola, S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
REFERENCE
1 (bases 1 to 3032)
Taylor, J. David., Kimmerly, W.J., Nelson, A.J., Gollivski, M.M.,
Rubino, M.A., Nelson, P.J., Rivers, P.R., Tortorella-Miller, J.,
Listebeebe, S., Ashanti, C., Altshuler, G., Mamola, S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
TITLE Direct Submission
Submitted (22-MAY-2000) Departments of Genome Sciences and
Bioinformatics, Genes Directorate, Glaxo Wellcome, Inc., 5 Moore
Drive, Research Triangle Park, North Carolina 27709-3398, USA
FEATURES
SOURCE
1..3032
/organism="Staphylococcus epidermidis"
/strain="SK1"
/db_xref="taxon:1282"
/clone="step.1028c03"
BASE COUNT 939 a 600 c 422 g 1071 t
ORIGIN
Query Match 24.2%; Score 16; DB 1; Length 1613;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GY 29 TAAAAACCGTAGAT 44
DB 3026 TAAAAACCGTAGAT 3011
RESULT 43
AX14520/c
LOCUS
DEFINITION
Sequence 3924 from patent W00134809.
ACCESSION
AX145202
VERSION
AX145202.1 GI:14283767
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequence.

FEATURES Location/Qualifiers

Source

1..523

/organism="unknown"

BASE COUNT 152 a 102 c 113 g 156 t

ORIGIN

Query Match 24.2% Score 16; DB 6; Length 523;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGGTAAAA 33

DB 230 CGACAAACGGTAAAA 245

RESULT 37 AR007434 535 bp DNA linear PAT 04-DEC-1998

LOCUS AR007434 Sequence 46 from patent US 5750497.

ACCESSION AR007434

VERSION AR007434.1 GI:3966918

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT 156 a 106 c 107 g 166 t

ORIGIN

Query Match 24.2% Score 16; DB 6; Length 535;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 18 CGACAAACGGTAAAA 33

DB 227 CGACAAACGGTAAAA 242

RESULT 38 AR007436 538 bp DNA linear PAT 04-DEC-1998

LOCUS AR007436 Sequence 49 from patent US 5750497.

ACCESSION AR007436

VERSION AR007436.1 GI:3966920

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT 156 a 107 c 107 g 168 t

ORIGIN

Query Match 24.2% Score 16; DB 6; Length 538;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGGTAAAA 33

DB 227 CGACAAACGGTAAAA 242

RESULT 39

AX105687 736 bp DNA linear PAT 30-APR-2001

LOCUS AX105687 Sequence 2 from Patent WO0124811.

ACCESSION AX105687

VERSION AX105687.1 GI:13921709

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT 200 a 170 c 160 g 206 t

ORIGIN

Query Match 24.2% Score 16; DB 6; Length 736;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 18 CGACAAACGGTAAAA 33

DB 158 CGACAAACGGTAAAA 173

RESULT 40 AX079100 1168 bp DNA linear PAT 22-FEB-2001

LOCUS AX079100 Sequence 21 from Patent WO0107591.

ACCESSION AX079100

VERSION AX079100.1 GI:13158674

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

BASE COUNT 242 a 382 c 356 g 188 t

ORIGIN

Query Match 24.2% Score 16; DB 6; Length 1168;

Best Local Similarity 100.0%; Pred. No. 64;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CGTTCGACAAACGGT 29

DB 566 CGTTCGACAAACGGT 551

RESULT 41 DB85545 1613 bp DNA linear PAT 14-APR-2000

LOCUS DB85545 Yeast chk1 and ucbb4 DNA, partial and complete cds.

ACCESSION DB85545

VERSION DB85545.1 GI:2190253

KEYWORDS

ucbb4; ucbb4; protein kinase; chk1.

PF000095_AHC_113un*

Query Match 25.8%; Score 17; DB 1; Length 282183;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AAAAAAGCTATGATGAC 47
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DB 266551 AAAAAAGCTATGATGAC 266535

RESULT 42
LOCUS AR151513 61 bp DNA
DEFINITION Sequence 10 from patent US 6232095.
ACCESSION AR151513
VERSION AR151513.1 GI:15117564
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 61)
AUTHORS Kameo, E.B., Holloman, W.K. and Gerhold, D.
TITLE Recombinant helix modification recognition proteins and uses thereof
JOURNAL Patent: US 6232095-A 10 15 MAY 2001;
FEATURES
Source location/Qualifiers
BASE COUNT 16 a 13 c 13 g 19 t
ORIGIN

Query Match 24.2%; Score 16; DB 6; Length 61;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TCCATCAATTCAGCT 65
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DB 47 TCCATCAATTCAGCT 52

RESULT 43
LOCUS AR007430 511 bp DNA
DEFINITION Sequence 40 from patent US 5750497.
ACCESSION AR007430
VERSION AR007430.1 GI:3966914
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 511)
AUTHORS Havelund, S., Halstr. o slashed, M.J., Jonassen, I., Andersen, A. Sloth, and Markussen, J.
TITLE Acylated insulin
JOURNAL Patent: US 5750497-A 40 12 MAY 1998;
FEATURES
Source location/Qualifiers
BASE COUNT 151 a 98 c 104 g 156 t
ORIGIN

Query Match 24.2%; Score 16; DB 6; Length 511;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGCTAAAA 33
|||||
DB 227 CGACAAACGCTAAAA 242

RESULT 34
LOCUS AR007416 523 bp DNA
DEFINITION Sequence 19 from patent US 5750497.
ACCESSION AR007416
VERSION AR007416.1 GI:3966900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 523)
AUTHORS Havelund, S., Halstr. o slashed, M.J., Jonassen, I., Andersen, A. Sloth, and Markussen, J.
TITLE Acylated insulin
JOURNAL Patent: US 5750497-A 19 12 MAY 1998;
FEATURES
Source location/Qualifiers
BASE COUNT 158 a 103 c 101 g 161 t
ORIGIN

Query Match 24.2%; Score 16; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGCTAAAA 33
|||||
DB 230 CGACAAACGCTAAAA 245

RESULT 35
LOCUS AR007426 523 bp DNA
DEFINITION Sequence 34 from patent US 5750497.
ACCESSION AR007426
VERSION AR007426.1 GI:3966910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 523)
AUTHORS Havelund, S., Halstr. o slashed, M.J., Jonassen, I., Andersen, A. Sloth, and Markussen, J.
TITLE Acylated insulin
JOURNAL Patent: US 5750497-A 34 12 MAY 1998;
FEATURES
Source location/Qualifiers
BASE COUNT 160 a 101 c 104 g 158 t
ORIGIN

Query Match 24.2%; Score 16; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGCTAAAA 33
|||||
DB 240 CGACAAACGCTAAAA 245

RESULT 36
LOCUS AR007432 523 bp DNA
DEFINITION Sequence 43 from patent US 5750497.
ACCESSION AR007432
VERSION AR007432.1 GI:3966916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 523)
AUTHORS Havelund, S., Halstr. o slashed, M.J., Jonassen, I., Andersen, A. Sloth, and Markussen, J.
TITLE Acylated insulin
JOURNAL Patent: US 5750497-A 43 12 MAY 1998;

LOCUS AR007416 523 bp DNA
DEFINITION Sequence 19 from patent US 5750497.
ACCESSION AR007416
VERSION AR007416.1 GI:3966900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 523)
AUTHORS Havelund, S., Halstr. o slashed, M.J., Jonassen, I., Andersen, A. Sloth, and Markussen, J.
TITLE Acylated insulin
JOURNAL Patent: US 5750497-A 19 12 MAY 1998;
FEATURES
Source location/Qualifiers
BASE COUNT 158 a 103 c 101 g 161 t
ORIGIN

Query Match 24.2%; Score 16; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGCTAAAA 33
|||||
DB 230 CGACAAACGCTAAAA 245

RESULT 35
LOCUS AR007426 523 bp DNA
DEFINITION Sequence 34 from patent US 5750497.
ACCESSION AR007426
VERSION AR007426.1 GI:3966910
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 523)
AUTHORS Havelund, S., Halstr. o slashed, M.J., Jonassen, I., Andersen, A. Sloth, and Markussen, J.
TITLE Acylated insulin
JOURNAL Patent: US 5750497-A 34 12 MAY 1998;
FEATURES
Source location/Qualifiers
BASE COUNT 160 a 101 c 104 g 158 t
ORIGIN

Query Match 24.2%; Score 16; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGACAAACGCTAAAA 33
|||||
DB 240 CGACAAACGCTAAAA 245

RESULT 36
LOCUS AR007432 523 bp DNA
DEFINITION Sequence 43 from patent US 5750497.
ACCESSION AR007432
VERSION AR007432.1 GI:3966916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 523)
AUTHORS Havelund, S., Halstr. o slashed, M.J., Jonassen, I., Andersen, A. Sloth, and Markussen, J.
TITLE Acylated insulin
JOURNAL Patent: US 5750497-A 43 12 MAY 1998;


```

* 88429: gap of unknown length
* 88429: contig of 4104 bp in length
* 92543: gap of unknown length
* 92543: contig of 4069 bp in length
* 96702: gap of unknown length
* 96801: contig of 3796 bp in length
* 100597: gap of unknown length
* 100598: contig of 2597 bp in length
* 100698: gap of unknown length
* 103495: gap of unknown length
* 103495: contig of 4368 bp in length
* 107764: gap of unknown length
* 107764: contig of 3097 bp in length
* 109560: gap of unknown length
* 109560: contig of 4272 bp in length
* 115332: gap of unknown length
* 115332: contig of 2641 bp in length
* 118064: gap of unknown length
* 118064: contig of 2907 bp in length
* 121066: gap of unknown length
* 121066: contig of 3420 bp in length
* 121166: gap of unknown length
* 124586: gap of unknown length
* 124586: contig of 3345 bp in length
* 128030: gap of unknown length
* 128030: contig of 2778 bp in length
* 140031: gap of unknown length
* 140031: contig of 2417 bp in length
* 140036: gap of unknown length
* 140036: contig of 1709 bp in length
* 142553: gap of unknown length
* 142553: contig of 1436 bp in length
* 144362: gap of unknown length
* 144362: contig of 1436 bp in length
* 145896: gap of unknown length
* 145896: contig of 3080 bp in length
* 149078: gap of unknown length
* 149078: contig of 2089 bp in length
* 151267: gap of unknown length
* 151267: contig of 1652 bp in length
* 153167: gap of unknown length
* 153167: contig of 1499 bp in length
* 154718: gap of unknown length
* 154718: contig of 1064 bp in length
* 155782: gap of unknown length
* 155782: contig of 1582 bp in length
* 157464: gap of unknown length
* 157464: contig of 1700 bp in length
* 159264: gap of unknown length
* 159264: contig of 1738 bp in length
* 161102: gap of unknown length
* 161102: contig of 1013 bp in length
* 162214: gap of unknown length
* 162214: contig of 1234 bp in length
* 163549: gap of unknown length
* 163549: contig of 1182 bp in length
* 164831: gap of unknown length
* 164831: contig of 1558 bp in length
* 166489: gap of unknown length
* 166489: contig of 1544 bp in length
* 168132: gap of unknown length
* 168132: contig of 1520 bp in length
* 169753: gap of unknown length
* 169753: contig of 1073 bp in length
* 170926: gap of unknown length
* 170926: contig of 1070 bp in length
* 172096: gap of unknown length
* 172096: contig of 1694 bp in length
* 174889: gap of unknown length
* 174889: contig of 1694 bp in length

```

```

FEATURES
  source
    * 173990 175362: contig of 1773 bp in length.
      Location/Qualifiers
        1..175362
          /organism="Rattus norvegicus"
          /db_xref="taxon:10116"
          /clone="CH230-182A20"
BASE COUNT  44086 a 41768 c 40485 g 41909 t 5114 others
ORIGIN
  Query Match      25.88; Score 17; DB 2; Length 175362;
  Best Local Similarity 100.0%; Prod. No. 17;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  1 TGCATCTGCATCCGTT 17
  |||||
  DB 155368 TGCATCTGCATCCGTT 155362

RESULT 31
CJ11168X/c
LACUS      CJ11168X
DEFINITION Campylobacter jejuni NC011168 complete genome; segment 4/6.
ACCESSION  AL139077 AL111168
VERSION     AL139077.2 GI:6968444
KEYWORDS
SOURCE
  ORGANISM  Campylobacter jejuni.
             Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
             Campylobacter.
REFERENCE
  1 (bases 1 to 282183)
    Parkhill,J., Wren,B.W., Mungall,K., Kellley,T.M., Churcher,C.,
    Basham,D., Chillingworth,T., Davies,R.M., Feltham,T., Holtroyd,S.,
    Jagels,K., Karlyshev,A., Mout,R., Pallen,M.J., Penn,C.M.,
    Quail,M., Rajandream,M.A., Rutherford,K.M., Vanniel,A.,
    Whitehead,S. and Barrett,B.G.
    The genome sequence of the food-borne pathogen Campylobacter jejuni
    reveals hypervariable sequences
    Nature 403 (6770), 665-668 (2000)
20150912
2 (bases 1 to 282183)
  Parkhill,J.
  Direct Submission
  Submitted (09-FEB-2000) Submitted on behalf of the Campylobacter
  sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
  Hinxton, Cambridgeshire CB10 1SA E-mail: parkhill@sanger.ac.uk
  Notes:
  Details of C. jejuni sequencing at the Sanger Centre are available
  on the World Wide Web.
  (URL: http://www.sanger.ac.uk/projects/c\_jejuni/).
  Location/Qualifiers
    1..282183
      /organism="Campylobacter jejuni"
      /strain="NCTC 11168"
      /db_xref="taxon:197"
      /complement(43..1443)
      /gene="Cj1009c"
      /complement(43..1443)
      /gene="Cj1009c"
      /note="Cj1009c, unknown, len: 466 aa; 29.1% identity to
      Hpo282"
      /codon_start=1
      /transl_table=11
      /product="hypothetical protein Cj1009c"
      /protein_id="CAJ73265.1"
      /db_xref="GI:6968445"
      /translation="MNNLLIDJLLAKHLERLTFKGLGYFTVVCNSKNNNT
      SSKETIDHFDPTSTARLENIISKPKQATFMQDEETKSTFALRSNPRIETIM
      DFNLGVNDTHANLADARTLSRRMDLPIDALTAQYIGLGVGEIMEVKTFAGSTFA
      YRHLSIIOQRKRVYLIVANSKIVPKSPVLENDLSLIVGDPVIVLSITNIRKA
      GQPMPEFGSNVALIDMKRMNOMQERVLDTTLATPKRSNKRFFHIVNPRIATVWE
      KIKKLSDEKGEVGFYNTDEKQISMLQNDNDIGLVVDIKNEFEKQAFPIKIPIM
      KVGESAPDELKFTIISADESTLENNAVLTIDSKQIDPVILYYYNPNQNTTME
      YFSLSKIDKNIGIILNNKNDENPLNTLDYRDIDLPSPVQKELLNDFANNTSLNIN

```


NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

FEATURES

SOURCE

1. 163156
 /organism="Oryza sativa"
 /cultivar="Nipponbare"
 /db_xref="taxon:4530"
 /chromosome="2"
 /clone="OJ1267.F10"

BASE COUNT 45475 d 32642 c 32750 g 52239 t 50 others

ORIGIN

Query Match 25.8%; Score 17; DB 2; Length 163156;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GACAAACGCTAAAAA 35
 ||||||||||||||||
 Db 56208 GACAAACGCTAAAAA 56224

RESULTS

AC097220/c

AC097220 175362 bp DNA linear HTG 20-DEC-2001
 Rattus norvegicus clone CH230-182A20, *** SEQUENCING IN PROGRESS

*** 51 unordered pieces.

AC097220 GI:17974120

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 175362)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alstbrooks, S.L., Amaral, H.C., Are, J.R., Banks, T., Barbieri, J., Beaton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burich, P., Burkett, C., Burrell, K.L., Byrd, N.C., Caron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dabonne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delawalle, K.J., Draper, H., Dunn, A.L., Ding, Y., Dinh, H.H., Douthett, K.J., Dwyer, J., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, J., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hayes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoque, M., Holloway, C., Hollins, B., Homi, F., Howard, S., Huber, J., Hulys, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jordan, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovari, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, Z., Lichtenberg, O., Liu, C., Liu, G., Liu, W., Lonsberg, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, F., Mashiney, F., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nookanxo, S., Nquyen, M., Okunoye, G., Otaguene, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Plickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Ruiz, S., Savery, G., Schorer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I., Sodergren, E., Sonnik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swalek, A., Taber, P., Tameris, A., Tameris, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Teliford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vilson, K., Wall, R., Wang, S., Ward, Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wlezyk, R., Wooten, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished
 2 (bases 1 to 175362)
 Morley, K.C.
 Direct Submission
 Submitted (12-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Dec 20, 2001 this sequence version replaced gi:17062578.

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GLSM

Center clone name: CH230-182A20

Summary Statistics

Assembly program: Phrap; version 0.990329first call to

findhaplolist

Consensus quality: 151852 bases at least Q40

Consensus quality: 157696 bases at least Q30

Consensus quality: 163100 bases at least Q20

Estimated insert size: 156934; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; aacrose-fp estimation

Quality coverage: 2.4x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 51 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 11433: contig of 11433 bp in length

11434 11533: gap of unknown length

11534 23019: contig of 11486 bp in length

23020 23119: gap of unknown length

23120 28445: contig of 5326 bp in length

28446 28545: gap of unknown length

28546 35047: contig of 6502 bp in length

35048 35147: gap of unknown length

35148 39726: contig of 4579 bp in length

39727 39827: gap of unknown length

39828 45920: contig of 6094 bp in length

45921 46020: gap of unknown length

46021 51618: contig of 5598 bp in length

51619 51718: gap of unknown length

51719 57861: contig of 6143 bp in length

57862 57962: gap of unknown length

57963 62845: contig of 4884 bp in length

62846 62945: gap of unknown length

62946 67809: contig of 4764 bp in length

67810 67910: gap of unknown length

67911 72298: contig of 4489 bp in length

72299 72399: gap of unknown length

72400 77865: contig of 5467 bp in length

77866 77965: gap of unknown length

77966 82802: contig of 4837 bp in length

82803 82902: gap of unknown length

82903 88328: contig of 5426 bp in length

14487 14586: gap of unknown length
 14587 14620: contig of 1434 bp in length
 18021 18120: gap of unknown length
 18121 22992: contig of 4872 bp in length
 22993 23092: gap of unknown length
 23093 25604: contig of 2512 bp in length
 25605 25704: gap of unknown length
 25705 28744: contig of 3039 bp in length
 28744 28844: gap of unknown length
 32166 32265: contig of 3322 bp in length
 32266 34785: contig of 2520 bp in length
 34786 34885: gap of unknown length
 34886 37354: contig of 2469 bp in length
 37355 37454: gap of unknown length
 37455 40784: contig of 3310 bp in length
 40785 40884: gap of unknown length
 40885 43725: contig of 2841 bp in length
 43726 43825: gap of unknown length
 43826 47154: contig of 3429 bp in length
 47155 47254: gap of unknown length
 47255 50670: contig of 3416 bp in length
 50671 50771: gap of unknown length
 50771 54398: contig of 3528 bp in length
 54399 54499: gap of unknown length
 54499 57179: contig of 2781 bp in length
 57180 57279: gap of unknown length
 57280 58994: contig of 1715 bp in length
 58995 59094: gap of unknown length
 59095 61619: contig of 2525 bp in length
 61620 61720: gap of unknown length
 61720 63859: contig of 2140 bp in length
 63860 63960: gap of unknown length
 63960 66483: contig of 2424 bp in length
 66484 68944: gap of unknown length
 68945 68994: contig of 2411 bp in length
 68995 71805: contig of 2811 bp in length
 71806 71905: gap of unknown length
 71906 74985: contig of 3080 bp in length
 74986 75085: gap of unknown length
 75086 77240: contig of 2055 bp in length
 77241 77341: gap of unknown length
 77341 79612: contig of 2372 bp in length
 79613 79712: gap of unknown length
 79713 82040: contig of 2328 bp in length
 82041 83804: gap of unknown length
 83805 83905: gap of unknown length
 83905 86146: contig of 2242 bp in length
 86147 86246: gap of unknown length
 86247 87807: contig of 1471 bp in length
 87808 89456: contig of 1549 bp in length
 89457 89456: gap of unknown length
 89457 91190: contig of 1734 bp in length
 91191 91290: gap of unknown length
 91291 91364: contig of 1974 bp in length
 91365 94365: gap of unknown length
 94365 95051: contig of 1687 bp in length
 95052 95151: gap of unknown length
 95152 96667: contig of 1516 bp in length
 96668 97996: gap of unknown length
 97997 98096: gap of unknown length
 98097 100872: contig of 2776 bp in length
 100873 100972: gap of unknown length
 100973 102483: contig of 1511 bp in length
 102484 104616: gap of unknown length
 104617 104716: gap of unknown length
 104717 105910: contig of 1194 bp in length
 105911 106010: gap of unknown length

106011 107403: contig of 1293 bp in length
 107404 107404: gap of unknown length
 107404 109894: contig of 2491 bp in length
 109895 109994: gap of unknown length
 109995 111925: contig of 1931 bp in length
 111926 112025: gap of unknown length
 112026 114199: contig of 2174 bp in length
 114200 114299: gap of unknown length
 114300 115738: contig of 1439 bp in length
 115739 115838: gap of unknown length
 115839 115930: contig of 1752 bp in length
 115931 117591: gap of unknown length
 117592 119426: contig of 1736 bp in length
 119427 119526: gap of unknown length
 119527 120857: contig of 1331 bp in length
 120858 120957: gap of unknown length
 120958 122635: contig of 1628 bp in length
 122636 122735: gap of unknown length
 122736 123872: contig of 1137 bp in length
 123873 123972: gap of unknown length
 123973 125798: contig of 1826 bp in length
 125799 125898: gap of unknown length
 125899 126939: contig of 1041 bp in length
 126940 127039: gap of unknown length
 127040 128753: contig of 1714 bp in length
 128754 128853: gap of unknown length
 128854 130069: contig of 1216 bp in length
 130070 130169: gap of unknown length
 130170 131575: contig of 1406 bp in length
 131576 131675: gap of unknown length
 131676 133752: contig of 2076 bp in length
 133752 133851: gap of unknown length
 133852 135254: contig of 1403 bp in length
 135255 135355: gap of unknown length
 135355 136789: contig of 1435 bp in length

Query Match 25.8% Score 17: DB 2: Length 154049;
 Best local Similarity 100.0%; Prod. No. 17;
 Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Oy 17 TCGACAAACGTAAAA 33
 DB 136487 TCGACAAACGTAAAA 136371

RESULT 29
 APO04085
 LOCUS
 DEFINITION
 Oryza sativa chromosome 2, clone: OJ1267_F10, *** SEQUENCING IN
 PROGRESS ***; in ordered pieces.

ACCESSION
 APO04085
 VERSION
 APO04085.1 GI:15281364
 KEYWORDS
 HTGS_PHASE2.
 SOURCE
 Oryza sativa
 ORGANISM
 Oryza sativa

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae:
 Ehrhartoideae: Oryzoae: Oryza.
 1 (bases 1 to 163156)
 Sasaki, T., Matsumoto, T. and Yamamoto, K.

REFERENCE
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Oryza sativa nipponbare(GAS) genomic DNA, chromosome 2, BAC
 clone: OJ1267_F10
 Published Only in Database (2001) In press

JOURNAL
 REFERENCE
 2 (bases 1 to 163156)
 Submitted (22-AUG-2001) Takuji Sasaki, National Institute of
 Agricultural Resources, Rice Genome Research Program, Kanonada
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail: tsasaki@nias.affrc.go.jp, URL: http://rqp.dna.affrc.go.jp/,
 Tel: 81-298-38-7441, Fax: 81-298-38-7468)
 The nucleotide sequence of this BAC clone was generated by
 combining Monsanto and RGP-Japan sequencing data.

COMMENT
 The nucleotide sequence of this BAC clone was generated by
 combining Monsanto and RGP-Japan sequencing data.

```

* 38987 39713: contig of 727 bp in length
* 39714 39813: gap of 100 bp
* 39814 40525: contig of 712 bp in length
* 40526 40625: gap of 100 bp
* 40626 41316: contig of 691 bp in length
* 41317 41416: gap of 100 bp
* 41417 42119: contig of 703 bp in length
* 42120 42219: gap of 100 bp
* 42220 42932: contig of 713 bp in length
* 42933 43032: gap of 100 bp
* 43033 43754: contig of 722 bp in length
* 43755 43854: gap of 100 bp
* 43855 44578: contig of 724 bp in length
* 44579 44678: gap of 100 bp
* 44679 45394: contig of 716 bp in length
* 45395 45494: gap of 100 bp
* 45495 46225: contig of 731 bp in length
* 46226 46325: gap of 100 bp
* 46326 47057: contig of 732 bp in length
* 47058 47157: gap of 100 bp
* 47158 47879: contig of 722 bp in length
* 47880 47979: gap of 100 bp
* 47980 48660: contig of 681 bp in length
* 48661 48760: gap of 100 bp
* 48761 49472: contig of 712 bp in length
* 49473 49572: gap of 100 bp
* 49573 50279: contig of 707 bp in length
* 50280 50379: gap of 100 bp
* 50380 51093: contig of 714 bp in length
* 51094 51193: gap of 100 bp
* 51194 51883: contig of 690 bp in length
* 51884 51983: gap of 100 bp
* 51984 52699: contig of 716 bp in length
* 52700 52799: gap of 100 bp
* 52800 53615: contig of 716 bp in length
* 53616 53615: gap of 100 bp
* 53616 54342: contig of 727 bp in length
* 54343 54442: gap of 100 bp
* 54443 55174: contig of 732 bp in length
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Best Local Similarity 100.00; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 31846 AAAAAACCGTAGATTA 31862

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LOCUS
DEFINITION
Rattus norvegicus clone CH230-114N22, *** SEQUENCING IN PROGRESS
***, 71 unordered pieces.
AC106377
AC106377.1 GI:18138898
KEYWORDS
HTG: HTCS_PHASE1.
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

```

REFERENCE
1 (bases 1 to 154049)
Muzny D.M., Adams C., Adio-Obunola B., Allisman F.R., Allen C.,
Alstooks S.L., Amaratunga H.C., Are, J.R., Banks T., Barabara, D.,
Benton, J., Bimage K., Blankenship K., Bonnin, D., Bouck, J.,
Bowle, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burke, P., Burkett, C., Butrell, K.L., Byrd, N.C., Cartron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, L., Christopoulos, C., Cleveland, C.D., Cox, C.,

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TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL
COMMENT

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Coyle M.D., Dathorne S.R., David R., Davila M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinu, H.H., Douthwaite, R.J., Dreher, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, Y., Garcia, A., Garner, T.,
Garza, N., Gill, R., Correll, J.H., Guera, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hones, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Bulky, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudan, S., Karlsson, E., Kelly, S., Khan, J., King, L., Korval, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewy, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulsgaard, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Manu, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mashimye, E., McLeod M.P., Meador, M.,
Mel, G., Metzger, M., Miner, G., Miner, G., Mitchell, T., Mohabat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Ogih, M., Okwono, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojokokan, I., Rolfe, M.,
Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shooshari, N.,
Sisson, I., Sodergren, E., Soneike, T., Sparks, A., Stanley, H.,
Stone, H., Sutton, A., Swack, A., Taber, P., Tamara, A., Tamara, K.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Wallington, S., Williams, G., Williamson, A., Wiscow, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Welnsstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 154049)
Morley, K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
-----
Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GKZ
Center clone name: CH230-114N22
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Summary Statistics
Assembly program: Phrap; version 0.990329first call to
findPhrapList
Consensus quality: 114472 bases at least Q40
Consensus quality: 124676 bases at least Q30
Consensus quality: 133577 bases at least Q20
Estimated insert size: 117794; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; average-ip estimation
Quality coverage: 1.3x in Q20 bases; sum-of-contigs estimation
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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/centbank_drift_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 71 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 4766: contig of 4766 bp in length
* 4767 4866: gap of unknown length
* 4867 10388: contig of 5522 bp in length
* 10389 10488: gap of unknown length
* 10489 14486: contig of 3998 bp in length

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JOURNAL,
REFERENCE
ALPHABETS

Unpublished
2 (pages 1 to 567566)

Alfaro, R., Hinton, L., Neshum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastian, V., Boguslavsky, L., Borkholder, H., Brown, A., Camarata, J., Campiano, A., Chang, J., Charata, B., Chepel, Y., Colangelo, M., Collins, S., Collimore, A., Cook, A., Cooke, P., DeAngelis, K., Dewar, K., Diaz, J., S., Dodge, S., Fato, S., Ferrelia, P., Fitzhugh, W., Gage, D., Galagan, J., Gardy, S., Gindoff, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Haines, H., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroix, K., Lamatez, R., Lander, S., T., Lohovsky, J., Leavitt, R., Liu, G., MacLean, C., MacDonald, P., Major, J., Margalit, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneses, L., Mihova, T., Miranda, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Patterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Risc, C., Rogov, P., Roman, J., Rosotti, M., Roy, A., Santos, R., Schaner, S., Schuppach, R., Seaman, S., Sorey, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Toplak, K., Travers, M., Travis, N., Triggilio, J., Vassiliou, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, H., Zaitoun, J., Zambek, B., Zimmer, A. and Zody, M.

Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIMR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu

Project Information
Center project name: L20402
Center clone name: 207.L.14

NOTE: This record contains 70 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

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12955	13054:	gap of	100 bp	in	length
13055	13733:	contig of 679 bp	in	length	
13734	13833:	gap of	100 bp	in	length
13834	14556:	contig of 723 bp	in	length	
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14657	15375:	contig of 719 bp	in	length	
15376	15475:	gap of	100 bp	in	length
15476	16163:	contig of 688 bp	in	length	
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16981	17080:	gap of	100 bp	in	length
17081	17788:	contig of 708 bp	in	length	
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22674	22773:	gap of	100 bp	in	length
22774	23473:	contig of 706 bp	in	length	
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25105	25204:	gap of	100 bp	in	length
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25892	25991:	gap of	100 bp	in	length
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32508	33224:	contig of 717 bp	in	length	
33225	33324:	gap of	100 bp	in	length
33325	34021:	contig of 697 bp	in	length	
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34827	34928:	gap of	100 bp	in	length
34927	35630:	contig of 704 bp	in	length	
35631	35730:	gap of	100 bp	in	length
35731	36444:	contig of 712 bp	in	length	
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38060	38155:	gap of	100 bp	in	length
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CY 17 TCGCACAAACGCGTAATAA 34
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db 125 TCGCACAAACGCGTAATAA 142

RESULT 27
AC107757
LOCUS
DEFINITION Mus musculus clone RP23-207J14, low-PASS SEQUENCE SAMPLING.
VERSION AC107757.1 GI:18308459
KEYWORDS HTG; HTGS_PHASE0.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases 1 to 56766)
Britten,B., Linton,L., Nusbaum,C. and Landier,F.
Mus musculus, clone Rp23-207J14

RESULT 24	AX203101	66 bp	DNA	Linear	PAT 30-AUG-2001
FEATURES	Sequence 9 from Patent W00153502.				
DEFINITION	AX203101				
ACCESSION	AX203101.1	GI:15392460			
VERSION	AX203101.1				
KEYWORDS					
SOURCE					
ORGANISM	Synthetic construct.				
REFERENCE	Synthetic construct.				
AUTHORS	artificial sequence.				
TITLE	1 (bases 1 to 66)				
JOURNAL	Brace, W.B. and Niu, X.				
	Novel root-primed promoter elements and methods of use				
	Patent: WO 0153502-A 9 26-JUL-2001;				
	PIONEER BI-BRED INTERNATIONAL, INC. (US)				
FEATURES	Local Ion/Qualifiers				
SOURCE	1..66				
BASE COUNT	7 a 9 c 9 g 11 t 30 others				
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DB	1 TCGATCTGGATCTCTTC 18				
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DEFINITION	Sequence 22 from Patent W00153502.				
ACCESSION	AX203114				
VERSION	AX203114.1	GI:15392475			
KEYWORDS					
SOURCE					
ORGANISM	Synthetic construct.				
REFERENCE	Synthetic construct.				
AUTHORS	artificial sequence.				
TITLE	1 (bases 1 to 66)				
JOURNAL	Brace, W.B. and Niu, X.				
	Novel root-primed promoter elements and methods of use				
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	PIONEER BI-BRED INTERNATIONAL, INC. (US)				
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Matches	18; conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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DB	2 GAAATCTGGATCTCTTCG 19				
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DEFINITION	Psychobaculum aerophilum strain IM2 section 182 of 201 of the				
ACCESSION	AF009927				
VERSION	AF009927.1	GI:18161597			

KEYWORDS	Pyrobaculum aerophilum.
SOURCE	Pyrobaculum aerophilum.
ORGANISM	Archaea: Crenarchaeota: Thermoprotei: Thermoproteales:
REFERENCE	Thermoproteaceae: Pyrobaculum.
AUTHORS	1 (bases 1 to 12645)
TITLE	Fitz-Gibbon, S.T., Ladner, H., Kim, U.-J., Stetter, K.O., Simon, M.L. and Miller, J.H.
JOURNAL	Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 99 (2), 984-989 (2002)
REFERENCE	2 (bases 1 to 12645)
AUTHORS	Fitz-Gibbon, S.T., Ladner, H., Kim, U.-J., Stetter, K.O., Simon, M.L. and Miller, J.H.
TITLE	Direct Submission
JOURNAL	Submitted (12-DEC-2001) Microbiology and Molecular Genetics, University of California, Los Angeles, 405 Hilgard Ave, Los Angeles, CA 90095-1489, USA
FEATURES	location/Qualifiers
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CDS	/db_xref="GI:18161599"
gene	/translation="MELIDKALELIRYPLGCSGIGKLPAGMCTGLNPEEGAKITLIMKLVDRKGRVLDNLALAKIRKPSRETSGLINDPACTGGGILKIVERYADVILALEGVEPRFEGFTGPRVDVRSSEVKKRLLTSGSEVKHINERIDKLLKILTKRVDKLPNIVYVMDLITGKASVSRNPLLEGVYLLKSRVSNARKFGKQKSTLMDKLVILREVGQKEHVIHVSCHESDARMALATIGLVEYELKQYDAIPFPMRQDIIKLPITPTKNEVRRIRIKERAKDILKHALVLSRELTVEELNRKIGESGKTIQYDTRRIRKILSPKKRNVVYELAMQGLSPRFELVYVQGGHLYKKEFHDGDKRTTSPVSELTTHLEVLRLIIVLSE"
gene	1749..3266
CDS	/gene="PAE3369"
gene	1749..3266
gene	/gene="PAE3369"
CDS	/note="Purines, pyrimidines, nucleosides, and nucleotides; putine ribonucleotide biosynthesis"
gene	/codon_start=1
CDS	/translation="GMP synthetase (glutamine-hydrolyzing)"
gene	/product="GMP synthetase (glutamine-hydrolyzing)"
CDS	/protein_id="AAL64871.1"
gene	/db_xref="GI:18161600"
gene	/translation="MEKLVVNFPGQVAHLIARRIRGVVAELASPEAVIRASKEEVAALVLSGSPSSVYEGAPDIDICITFALSKPVGLCYGHOMIAKLGKVRGKGVGKTIVLILVNDLPFGMKPEFAVMMSSDVEEPDGHVLAISNGYIAAKRKILYGVGVFHVHTSKGVNPNILKILAKISYMRQEDITRIVELISRGKQDILVGSVGVNSVYAVLLIKAVGRKAVPTIHGILPRGEPKASLKSIGTIVYITDAKRPFKRIEGVADCEKRRITIGTFPAVFSIDAVKQMNKAVYLAQGLTPDVHESGAVGAKIKISHNVGSLPMPLELLEPRFVYKDVYRIANAGIGPELVYVRRHPGPHAVRI

JOURNAL Patent: WO 0153502-A 13-26-JUL-2001;

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES Location/Qualifiers

SOURCE

1. 18
/organism="synthetic construct"

/db_xref="taxon:32630"

/note="primer"

BASE COUNT 4 a 5 c 4 g 5 t

Query Match 27.3%; Score 18; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 GTCCTACGATTCAGCTG 66

DB 1 GTCCTACGATTCAGCTG 18

RESULT 20

AX203096 64 bp DNA linear PAT 30-AUG-2001

LOCUS Sequence 4 from Patent WO0153502.

DEFINITION AX203096

ACCESSION AX203096.1 GI:15392455

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 64)

Novel root-preferred promoter elements and methods of use

JOURNAL

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES Location/Qualifiers

SOURCE

1. 64

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="random oligonucleotide"

BASE COUNT 16 a 13 c 17 g 18 t

ORIGIN

Query Match 27.3%; Score 18; DB 6; Length 64;

Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAGATCTGATCCGCTTC 18

DB 1 TGAGATCTGATCCGCTTC 18

RESULT 21

AX203100 64 bp DNA linear PAT 30-AUG-2001

LOCUS Sequence 8 from Patent WO0153502.

DEFINITION AX203100

ACCESSION AX203100.1 GI:15392459

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 64)

Novel root-preferred promoter elements and methods of use

AUTHORS

Bruce, W.B. and Niu, X.

JOURNAL

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES Location/Qualifiers

SOURCE

1. 64

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="random oligonucleotide"

BASE COUNT 22 a 11 c 16 g 15 t

ORIGIN

Query Match 27.3%; Score 18; DB 6; Length 64;

Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAGATCTGATCCGCTTC 18

DB 1 TGAGATCTGATCCGCTTC 18

RESULT 22

AX203097 65 bp DNA linear PAT 30-AUG-2001

LOCUS Sequence 5 from Patent WO0153502.

DEFINITION AX203097

ACCESSION AX203097.1 GI:15392456

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 65)

Novel root-preferred promoter elements and methods of use

AUTHORS

Bruce, W.B. and Niu, X.

JOURNAL

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES Location/Qualifiers

SOURCE

1. 65

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="random oligonucleotide"

BASE COUNT 16 a 14 c 17 g 18 t

ORIGIN

Query Match 27.3%; Score 18; DB 6; Length 65;

Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAGATCTGATCCGCTTC 18

DB 1 TGAGATCTGATCCGCTTC 18

RESULT 23

AX203099 65 bp DNA linear PAT 30-AUG-2001

LOCUS Sequence 7 from Patent WO0153502.

DEFINITION AX203099

ACCESSION AX203099.1 GI:15392458

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 65)

Novel root-preferred promoter elements and methods of use

AUTHORS

Bruce, W.B. and Niu, X.

JOURNAL

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES Location/Qualifiers

SOURCE

1. 65

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="random oligonucleotide"

BASE COUNT 19 a 13 c 18 g 15 t

ORIGIN

Query Match 27.3%; Score 18; DB 6; Length 65;

Best Local Similarity 100.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGAGATCTGATCCGCTTC 18

DB 1 TGAGATCTGATCCGCTTC 18

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|||||
IDB 1 TGAGATCTGATCGCTTCG 19
RESULT 15
AX203112
LOCUS AX203112 66 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 20 from Patent W00153502.
ACCESSION AX203112
VERSION AX203112.1 GI:15392473
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequence
REFERENCE
1 (bases 1 to 66)
AUTHORS Bruce, W.H. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patient: W0 0153502-A 20 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Source
1..66
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic sequences flanking a random oligonucleotide"
BASE COUNT 19 a 11 c 21 g 15 t
ORIGIN
Query Match 28.8%; Score 19; DB 6; Length 66;
Best local Similarity 100.0%; Pred. No. 0.79;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
IDB 1 TGAGATCTGATCGCTTCG 19
RESULT 16
AX203102
LOCUS AX203102 18 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 10 from Patent W00153502.
ACCESSION AX203102
VERSION AX203102.1 GI:15392461
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequence
REFERENCE
1 (bases 1 to 18)
AUTHORS Bruce, W.H. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patient: W0 0153502-A 10 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Source
1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer with BamH1 site"
BASE COUNT 4 a 4 c 5 g 6 t
ORIGIN
Query Match 27.8%; Score 18; DB 6; Length 18;
Best local Similarity 100.0%; Pred. No. 3.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
IDB 1 TGAGATCTGATCGCTTCG 18
RESULT 17
AX203103
LOCUS AX203103 18 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 11 from Patent W00153502.

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ACCESSION AX203103
VERSION AX203103.1 GI:15392462
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequence
REFERENCE
1 (bases 1 to 18)
AUTHORS Bruce, W.H. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patient: W0 0153502-A 11 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Source
1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer with KpnI site"
BASE COUNT 5 a 4 c 5 g 4 t
ORIGIN
Query Match 27.8%; Score 18; DB 6; Length 18;
Best local Similarity 100.0%; Pred. No. 3.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
IDB 18 GTCTACCAATTCAGCTG 66
IDB 18 GTCTACCAATTCAGCTG 1
49 GTCTACCAATTCAGCTG 66
RESULT 18
AX203104/C
LOCUS AX203104 18 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 12 from Patent W00153502.
ACCESSION AX203104
VERSION AX203104.1 GI:15392463
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequence
REFERENCE
1 (bases 1 to 18)
AUTHORS Bruce, W.H. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patient: W0 0153502-A 12 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Source
1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 6 a 5 c 4 g 3 t
ORIGIN
Query Match 27.8%; Score 18; DB 6; Length 18;
Best local Similarity 100.0%; Pred. No. 3.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
IDB 18 TGAGATCTGATCGCTTCG 18
RESULT 19
AX203105
LOCUS AX203105 18 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 13 from Patent W00153502.
ACCESSION AX203105
VERSION AX203105.1 GI:15392465
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequence
REFERENCE
1 (bases 1 to 18)
AUTHORS Bruce, W.H. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use

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FEATURES
Source
Location/Qualifiers
1..66
/db_xref="taxon:32630"
/note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 19 a 11 c 21 g 14 t 1 others

Query Match 36.4%; Score 24; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTACGCTCAGCAATTCAGCTG 66
|||||
DB 43 ATTACGCTCAGCAATTCAGCTG 66

RESULT 11
AX203113 66 bp DNA Linear PAT 30-AUG-2001
LOCUS Sequence 21 from Patent W00153502.
DEFINITION AX203113 GI:15392474
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
1 (bases 1 to 66)
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 0153502-A 21 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
1..66
/db_xref="taxon:32630"
/note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 20 a 12 c 20 g 13 t 1 others

Query Match 36.4%; Score 24; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTACGCTCAGCAATTCAGCTG 66
|||||
DB 43 ATTACGCTCAGCAATTCAGCTG 66

RESULT 12
AX203115 66 bp DNA Linear PAT 30-AUG-2001
LOCUS Sequence 23 from Patent W00153502.
DEFINITION AX203115
ACCESSION AX203115 GI:15392476
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
1 (bases 1 to 66)
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 0153502-A 23 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
1..66
/db_xref="taxon:32630"
/note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 19 a 12 c 22 g 13 t

Query Match 33.3%; Score 22; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 TACCGCTCAGCAATTCAGCTG 66
|||||
DB 45 TACCGCTCAGCAATTCAGCTG 66

RESULT 13
AX203106 65 bp DNA Linear PAT 30-AUG-2001
LOCUS Sequence 14 from Patent W00153502.
DEFINITION AX203106
ACCESSION AX203106 GI:15392467
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
1 (bases 1 to 65)
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 0153502-A 14 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
1..65
/db_xref="taxon:32630"
/note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 18 a 14 c 17 g 16 t

Query Match 30.3%; Score 20; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCGATCGCTTCA 20
|||||
DB 1 TGAGATCGATCGCTTCA 20

RESULT 14
AX203098 62 bp DNA Linear PAT 30-AUG-2001
LOCUS Sequence 6 from Patent W00153502.
DEFINITION AX203098
ACCESSION AX203098 GI:15392457
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
1 (bases 1 to 62)
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 0153502-A 6 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
1..62
/db_xref="taxon:32630"
/note="random oligonucleotide"

BASE COUNT 18 a 11 c 18 g 15 t

Query Match 28.8%; Score 19; DB 6; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCGATCGCTTCA 19

RESULT 6
AXZ03107
LOCUS AXZ03107 66 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 15 from Patent W00153502.
ACCESSION AXZ03107
VERSION AXZ03107.1 GI:15392468
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 15-26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
1..66
/organism="synthetic construct"
/db_xref="taxon:42630"
/note="synthetic sequences flanking a random oligonucleotide"
BASE COUNT 20 a 12 c 21 g 13 t
ORIGIN
Query Match 36.4%; Score 24; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 ATTACGCTCTACCAATTCAGCTG 66
|||||
DB 43 ATTACGCTCTACCAATTCAGCTG 66
RESULT 7
AXZ03108
LOCUS AXZ03108 66 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 16 from Patent W00153502.
ACCESSION AXZ03108
VERSION AXZ03108.1 GI:15392469
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 16-26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
1..66
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic sequences flanking a random oligonucleotide"
BASE COUNT 19 a 11 c 21 g 15 t
ORIGIN
Query Match 46.4%; Score 24; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 ATTACGCTCTACCAATTCAGCTG 66
|||||
DB 43 ATTACGCTCTACCAATTCAGCTG 66
RESULT 8
AXZ03109
LOCUS AXZ03109 66 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 17 from Patent W00153502.
ACCESSION AXZ03109
VERSION AXZ03109.1 GI:15392470
KEYWORDS

SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 17-26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
1..66
/organism="synthetic construct"
/db_xref="taxon:42630"
/note="synthetic sequences flanking a random oligonucleotide"
BASE COUNT 19 a 12 c 21 g 14 t
ORIGIN
Query Match 36.4%; Score 24; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 ATTACGCTCTACCAATTCAGCTG 66
|||||
DB 43 ATTACGCTCTACCAATTCAGCTG 66
RESULT 9
AXZ03110
LOCUS AXZ03110 66 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 18 from Patent W00153502.
ACCESSION AXZ03110
VERSION AXZ03110.1 GI:15392471
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 18-26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
1..66
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic sequences flanking a random oligonucleotide"
BASE COUNT 19 a 12 c 21 g 14 t
ORIGIN
Query Match 36.4%; Score 24; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 ATTACGCTCTACCAATTCAGCTG 66
|||||
DB 43 ATTACGCTCTACCAATTCAGCTG 66
RESULT 10
AXZ03111
LOCUS AXZ03111 66 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 19 from Patent W00153502.
ACCESSION AXZ03111
VERSION AXZ03111.1 GI:15392472
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 19-26-JUL-2001;

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Query Match          100.0%; Score 66; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.le-30;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCTGGATCCGTTTCGACAAACGGTAAAGCGGTAGATTACCGTCTCTACGAATT 60
    |||||||
Db 1 TGAGATCTGGATCCGTTTCGACAAACGGTAAAGCGGTAGATTACCGTCTCTACGAATT 60

QY 61 CAGCTG 66
    |||||||
Db 61 CAGCTG 66

RESULT 2
LOCUS      AX203116          66 bp      DNA      linear      PAT 30-AUG-2001
DEFINITION Sequence 24 from Patent WO0153502.
ACCESSION  AX203116
VERSION     AX203116.1 GI:15392477
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 66)
AUTHORS     Bruce,W.B. and Niu,X.
TITLE       Novel root-preferred promoter elements and methods of use
JOURNAL     PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES    Location/Qualifiers
             source
               1..66
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="synthetic sequences flanking a random
               oligonucleotide"
BASE COUNT  21 a 14 c 16 g 15 t

Query Match          100.0%; Score 66; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.le-30;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCTGGATCCGTTTCGACAAACGGTAAAGCGGTAGATTACCGTCTCTACGAATT 60
    |||||||
Db 1 TGAGATCTGGATCCGTTTCGACAAACGGTAAAGCGGTAGATTACCGTCTCTACGAATT 60

QY 61 CAGCTG 66
    |||||||
Db 61 CAGCTG 66

RESULT 3
LOCUS      AX2031095          66 bp      DNA      linear      PAT 30-AUG-2001
DEFINITION Sequence 3 from Patent WO0153502.
ACCESSION  AX2031095
VERSION     AX2031095.1 GI:15392454
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 66)
AUTHORS     Bruce,W.B. and Niu,X.
TITLE       Novel root-preferred promoter elements and methods of use
JOURNAL     PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES    Location/Qualifiers
             source
               1..66
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="random oligonucleotide"
BASE COUNT  22 a 14 c 15 g 15 t

Query Match          100.0%; Score 66; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.le-30;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCTGGATCCGTTTCGACAAACGGTAAAGCGGTAGATTACCGTCTCTACGAATT 60
    |||||||
Db 1 TGAGATCTGGATCCGTTTCGACAAACGGTAAAGCGGTAGATTACCGTCTCTACGAATT 60

QY 61 CAGCTG 66
    |||||||
Db 61 CAGCTG 66

RESULT 4
LOCUS      AX207072          26 bp      DNA      linear      PAT 30-AUG-2001
DEFINITION Sequence 25 from Patent WO0153476.
ACCESSION  AX207072
VERSION     AX207072.1 GI:15394865
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 26)
AUTHORS     Bruce,W.B. and Niu,X.
TITLE       Novel plant promoters and methods of use
JOURNAL     Patent: WO 0153476-A 25 26-JUL-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES    Location/Qualifiers
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               1..26
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="synthetic"
BASE COUNT  12 a 4 c 6 g 4 t

Query Match          39.4%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AAACGGTAAAAAGCGGTAGATTACC 48
    |||||||
Db 1 AAACGGTAAAAAGCGGTAGATTACC 26

RESULT 5
LOCUS      AX203093          66 bp      DNA      linear      PAT 30-AUG-2001
DEFINITION Sequence 1 from Patent WO0153502.
ACCESSION  AX203093
VERSION     AX203093.1 GI:15392451
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    artificial sequence.
REFERENCE   1 (bases 1 to 66)
AUTHORS     Bruce,W.B. and Niu,X.
TITLE       Novel root-preferred promoter elements and methods of use
JOURNAL     Patent: WO 0153502-A 1 26-JUL-2001;
            PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES    Location/Qualifiers
             source
               1..66
               /organism="synthetic construct"
               /db_xref="taxon:32630"
               /note="random oligonucleotide"
BASE COUNT  19 a 12 c 21 g 14 t

Query Match          36.4%; Score 24; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTACCGTCTCTACGAATTCAGCTG 66
    |||||||
Db 43 ATTACCGTCTCTACGAATTCAGCTG 66

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OM nucleic - nucleic search, using sw model

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(without alignments)
4591.252 Million cell updates/sec

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Perfect score: 66

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8: qb_pl.*

9: qb_pr.*

10: qb_ro.*

11: qb_sus.*

12: qb_sy.*

13: qb_un.*

14: qb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sus.*

28: em_un.*

29: em_vl.*

30: em_hfq_hum.*

31: em_hfq_inv.*

32: em_hfq_other.*

33: em_hfq_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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ALIGNMENTS

RESULT 1

AX203094

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS

TITLE

JOURNAL

FEATURES

source

AX203094 Sequence 2 from Patent WO0154502. 66 bp DNA 110041 PAT 10 AUG 2001

AX203094 AX203094.1 GI:15392453

synthetic construct.

synthetic construct

artificial sequence

1 (bases 1 to 66)

Bruce, W. H. and Niu, X.

Novel root-preferred promoter elements and methods of use

Patent: WO 0153502-A 2 26-JUL-2001;

PIONEER HI-BRED INTERNATIONAL, INC. (US)

Location/Qualifiers

1..66

/organism="synthetic construct"

/db_xref="taxon:42630"

/note="random oligonucleotide"

15 t

BASE COUNT 21 a 14 c 16 q 15 t

ORIGIN

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 5, 2002, 05:28:54 ; Search time 95.8147 Seconds
(without alignments)
1182.662 Million cell updates/sec

Title: US-09-766-113-2

Perfect score: 66

Sequence: 1 tgaatctggatcgttcga.....ccqctactcaatcagctg 66

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	66	AAS08433	A plant root-pre
2	66	100.0	66	AAS08453	A plant root-pre
3	43	50.0	66	AAS08434	A plant root-pre
4	26	39.4	26	AAH42733	A promoter element
5	24	36.4	66	AAS08432	A plant root-pre
6	24	36.4	66	AAS08446	A plant root-pre
7	24	36.4	66	AAS08447	A plant root-pre
8	24	36.4	66	AAS08448	A plant root-pre
9	24	36.4	66	AAS08450	A plant root-pre

10	22	33.3	66	22	AAS08452	A plant root-pre
11	20	30.4	65	22	AAS08445	A plant root-pre
12	19	28.8	62	22	AAS08437	A plant root-pre
13	19	28.8	66	22	AAS08449	A plant root-pre
14	18	27.3	18	22	AAS08441	A random oligonucleotide
15	18	27.3	18	22	AAS08442	A random oligonucleotide
16	18	27.3	18	22	AAS08443	A random oligonucleotide
17	18	27.3	18	22	AAS08444	A random oligonucleotide
18	18	27.3	64	22	AAS08435	A plant root-pre
19	18	27.3	64	22	AAS08439	A plant root-pre
20	18	27.3	65	22	AAS08436	A plant root-pre
21	18	27.3	65	22	AAS08438	A plant root-pre
22	18	27.3	66	22	AAS08440	A random oligonucleotide
23	18	27.3	66	22	AAS08451	A plant root-pre
24	16	24.2	462	23	AAS53852	Helicobacter pylori
25	16	24.2	1168	22	AAP60852	Pseudomonas sp exp
26	16	24.2	2731	23	ABL05397	Drosophila melanog
27	16	24.2	3032	22	AH54560	S. epidermidis gen
28	16	24.2	3246	22	AH53972	S. epidermidis gen
29	16	24.2	4019	22	AH54846	S. epidermidis gen
30	16	24.2	7345	23	ABL05396	Drosophila melanog
31	16	24.2	86584	21	AAF22292	BAC containing rep
32	15	22.7	36	13	AAQ24203	Transglutaminase p
33	15	22.7	44	22	AD03192	PCR primer #2 used
34	15	22.7	478	7	AAN60630	Beta-uroastrome
35	15	22.7	533	21	AA291620	E.coli promoter re
36	15	22.7	539	7	AAF55139	Sulfometuron methy
37	15	22.7	539	7	AAN60642	Beta-uroastrome
38	15	22.7	654	7	AAN60641	Beta-uroastrome
39	15	22.7	847	22	AA193990	Human neuroblastom
40	15	22.7	883	22	AA194316	Human neuroblastom
41	15	22.7	969	21	AA254037	Neisseria meningit
42	15	22.7	1104	22	AA254037	Neisseria meningit
43	15	22.7	1170	19	AA14265	Haemophilus influe
44	15	22.7	1457	22	AH19477	H. pylori GPR0 156
45	15	22.7	1550	23	ABL02975	Human nervous syst
						Drosophila melanog

ALIGNMENTS

RESULTS
AAS08433
ID AAS08433 standard; DNA: 66 BP.

AC AAS08433;

DT 26-SEP-2001 (first entry)

XX A plant root-preferred promoter element (RPE), RPE 14.

DE Root-preferred promoter element; RPE; abiotic stress; drought;
KW salinity; pesticide resistance; herbicide resistance; biotic stress;
KW disease resistance; fungal disease; bacterial disease; viral disease;
KW insect attack; nematode attack; RPE14; random oligonucleotide library;
KW ROL; ss.

OS Synthetic

XX Key Location/qualifiers

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FT /tag= a

FT /label= "5'_flanking_sequence"

FT misc_feature 19..48

FT /tag= b

FT /note= "Randomised sequence"

FT misc_feature 49..66

FT /tag= c

FT /label= "3'_flanking_sequence"

XX W0200153502-A2.

XX 26-JUL-2001.

PD

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XX 19-JAN-2001; 2001WO-US02011.
XX 21-JAN-2000; 2000US-0177473.
XX (PION-) PIONEER HI-BRED INT INC.
XX Bruce WB, Niu X;
XX WP1; 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements -
XX
XX Claim 5; Fig 1; 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 66 BP; 21 A; 14 C; 16 G; 15 T; 0 other;
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Best Local Similarity 100.0%; Pred. No. 4.8e-26;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAGATCTGGATCGGTCGACAAACGGTAAAAAGCGGTAGATTACCGTCTCTAGCAATT 60
DB 1 TGAGATCTGGATCGGTCGACAAACGGTAAAAAGCGGTAGATTACCGTCTCTAGCAATT 60
QY 61 CAGCTG 66
DB 61 CAGCTG 66
RESULT 2
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ID AAS08453 standard; DNA; 66 BP.
AC AAS08453;
XX
XX 26-SEP-2001 (first entry)
XX
XX A plant root-preferred promoter element (RPE), RPE 21.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE21; random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
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XX 19..48
XX /tag= b
XX /note= "Randomised sequence"

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XX WO200153502-A2.
XX 26-JUL-2001.
XX 19-JAN-2001; 2001WO-US02011.
XX 21-JAN-2000; 2000US-0177473.
XX (PION-) PIONEER HI-BRED INT INC.
XX Bruce WB, Niu X;
XX WP1; 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements -
XX
XX Example 1; Fig 1; 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 66 BP; 21 A; 14 C; 16 G; 15 T; 0 other;
XX
Query Match 100.0%; Score 66; DB 22; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.8e-26;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAGATCTGGATCGGTCGACAAACGGTAAAAAGCGGTAGATTACCGTCTCTAGCAATT 60
DB 1 TGAGATCTGGATCGGTCGACAAACGGTAAAAAGCGGTAGATTACCGTCTCTAGCAATT 60
QY 61 CAGCTG 66
DB 61 CAGCTG 66
RESULT 3
AAS08434
ID AAS08434 standard; DNA; 66 BP.
AC AAS08434;
XX
XX 26-SEP-2001 (first entry)
XX
XX A plant root-preferred promoter element (RPE), RPE 19.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE19; random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX

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FH Key Location/Qualifiers
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FT misc_feature 49..66
FT /tag- c
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XX
PN WO200153502-A2.
XX
FD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US02011.
XX
PR 21-JAN-2000; 2000US-0177473.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Bruce WB, Niu X;
XX
DR WPI: 2001-442261/47.
XX
CC Producing tissue-preferred promoter elements constructs for regulating
CC expression of nucleotide sequences in a plant comprises identifying and
CC isolating tissue-preferred promoter elements -
XX
PS Claim 5; Fig 1; 45pp; English.
XX
CC The sequence represents a plant root-preferred promoter element, RPE,
CC isolated from a random oligonucleotide library (ROL). The invention
CC concerns a method of identifying and isolating tissue-preferred promoter
CC elements comprising the use of a mixture of random oligonucleotides,
CC flanked by 5' and 3' flanking sequences, which hybridise to tissue-
CC specific plant nuclear proteins, isolating the complexes and PCR
CC amplifying the bound oligonucleotide. The method is used for isolating
CC tissue-specific promoters from plants, including but not limited to
CC root-specific promoters or root-preferred promoter elements (RPE). The
CC RPEs are useful in the genetic manipulation of a plant when operably
CC linked to a nucleotide sequence whose expression is to be controlled to
CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
CC temperature, salinity, pesticide and herbicide resistance) and biotic
CC stress (disease resistance, resistance to attack by fungi, bacteria,
CC viruses, insects and nematodes).
XX
SQ Sequence 66 BP; 22 A; 14 C; 15 G; 15 T; 0 Other;

Query Match 50.0%; Score 33; DB 22; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCTGGATCCGTCGACAAACGGTAAAA 33
   |||||||
Db 1 TGAGATCTGGATCCGTCGACAAACGGTAAAA 33

RESULT 4
AAH42733
ID AAH42733 standard; DNA; 26 BP.
XX
AC AAH42733;
XX
DT 01-OCT-2001 (first entry)
XX
DE A promoter element or transcription binding site.
XX
KW Promoter element; transcription binding site; plant promoter; SMPER;
KW synthetic multimeric promoter element region; gene expression;
KW insect resistance; herbicide resistance; ss.
XX
QS Synthetic.

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XX
PN WO200153476-A2.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US02024.
XX
PR 21-JAN-2000; 2000US-0177437.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Bruce WB, Niu X;
XX
DR WPI: 2001-476118/51.
XX
CC New plant promoters with synthetic multimeric promoter element regions,
CC useful in plant molecular biology, particularly in regulating gene
CC expression in plants to increase resistance against insects or
CC herbicides
XX
PS Example 1; Fig 1; 67pp; English.
XX
CC AAH42709-72 represent promoter elements or transcription binding sites.
CC They are used to construct synthetic multimeric promoter element
CC regions (SMPERs). The specification describes plant promoters which
CC comprise SMPERs. The plant promoters are useful in plant molecular
CC biology, particularly in regulating gene expression in plants. The
CC promoters are especially useful for transforming plants or plant cells,
CC e.g. to increase resistance against insects or herbicides.
XX
SQ Sequence 26 BP; 12 A; 4 C; 6 G; 4 T; 0 Other;

Query Match 39.4%; Score 26; DB 22; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 AAACGGTAAAAAGCGGTAGATTACC 48
   |||||||
Db 1 AAACGGTAAAAAGCGGTAGATTACC 26

RESULT 5
AAS08432
ID AAS08432 standard; DNA; 66 BP.
XX
AC AAS08432;
XX
DT 26-SEP-2001 (first entry)
XX
DE A plant root-preferred promoter element (RPE), RPE 15.
XX
KW Root-preferred promoter element; RPE; abiotic stress; drought;
KW salinity; pesticide resistance; herbicide resistance; biotic stress;
KW disease resistance; fungal disease; bacterial disease; viral disease;
KW insect attack; nematode attack; RPE15; random oligonucleotide library;
KW ROL; ss.
XX
QS Synthetic.
XX
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XX
PN WO200153502-A2.
XX
PD 26-JUL-2001.

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XX 19-JAN-2001; 2001WO-US02011.
 XX 21-JAN-2000; 2000US-0177473.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Bruce WB, Niu X;
 XX WPI: 2001 442261/47.
 XX Producing tissue-preferred promoter elements constructs for regulating
 PT expression of nucleotide sequences in a plant comprises identifying and
 PT isolating tissue-preferred promoter elements.
 XX Claim 5; Fig 1; 45pp; English.
 XX The sequence represents a plant root-preferred promoter element, RPE,
 CC isolated from a random oligonucleotide library (ROL). The invention
 CC concerns a method of identifying and isolating tissue-preferred promoter
 CC elements comprising the use of a mixture of random oligonucleotides,
 CC flanked by 5' and 3' flanking sequences, which hybridise to tissue-
 CC specific plant nuclear proteins, isolating the complexes and PCR
 CC amplifying the bound oligonucleotide. The method is used for isolating
 CC tissue-specific promoters or root-preferred promoter elements (RPE). The
 CC RPEs are useful in the genetic manipulation of a plant when operably
 CC linked to a nucleotide sequence whose expression is to be controlled to
 CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
 CC temperature, salinity, pesticide and herbicide resistance) and biotic
 CC stress (disease resistance, resistance to attack by fungi, bacteria,
 CC viruses, insects and nematodes).
 XX Sequence 66 BP; 19 A; 12 C; 21 G; 14 T; 0 other;
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Query Match 36.4%; Score 24; DB 22; Length 66;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 ATTACCGTCTACGAATTCAGCTG 66
 |||||
 DB 43 ATTACCGTCTACGAATTCAGCTG 66

RESULT 6
 AAS08446
 ID AAS08446 standard; DNA; 66 BP.
 AC AAS08446;
 XX 26-SEP-2001 (first entry)
 XX A plant root-preferred promoter element (RPE), RPE 18.

XX Root-preferred promoter element; RPE; abiotic stress: drought;
 KW salinity; pesticide resistance; herbicide resistance; biotic stress;
 KW disease resistance; fungal disease; bacterial disease; viral disease;
 KW insect attack; nematode attack; RPE18; random oligonucleotide library;
 KW ROL; ss.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
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 FT 19..48
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PN WO200153502-A2.
 XX 26-JUL-2001.
 XX 19-JAN-2001; 2001WO-US02011.
 XX PF 21-JAN-2000; 2000US-0177473.
 XX PR 21-JAN-2000; 2000US-0177473.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Bruce WB, Niu X;
 XX WPI: 2001-442261/47.
 XX Producing tissue-preferred promoter elements constructs for regulating
 PT expression of nucleotide sequences in a plant comprises identifying and
 PT isolating tissue-preferred promoter elements.
 XX Example 1; Fig 1; 45pp; English.
 XX The sequence represents a plant root-preferred promoter element, RPE,
 CC isolated from a random oligonucleotide library (ROL). The invention
 CC concerns a method of identifying and isolating tissue-preferred promoter
 CC elements comprising the use of a mixture of random oligonucleotides,
 CC flanked by 5' and 3' flanking sequences, which hybridise to tissue-
 CC specific plant nuclear proteins, isolating the complexes and PCR
 CC amplifying the bound oligonucleotide. The method is used for isolating
 CC tissue-specific promoters from plants, including but not limited to
 CC root-specific promoters or root-preferred promoter elements (RPE). The
 CC RPEs are useful in the genetic manipulation of a plant when operably
 CC linked to a nucleotide sequence whose expression is to be controlled to
 CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
 CC temperature, salinity, pesticide and herbicide resistance) and biotic
 CC stress (disease resistance, resistance to attack by fungi, bacteria,
 CC viruses, insects and nematodes).
 XX Sequence 66 BP; 20 A; 12 C; 21 G; 13 T; 0 other;
 SQ

Query Match 36.4%; Score 24; DB 22; Length 66;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTACCGTCTACGAATTCAGCTG 66
 |||||
 DB 43 ATTACCGTCTACGAATTCAGCTG 66

RESULT 7
 AAS08447
 ID AAS08447 standard; DNA; 66 BP.
 AC AAS08447;
 XX 26-SEP-2001 (first entry)
 XX A plant root-preferred promoter element (RPE), RPE 42.
 XX Root-preferred promoter element; RPE; abiotic stress: drought;
 KW salinity; pesticide resistance; herbicide resistance; biotic stress;
 KW disease resistance; fungal disease; bacterial disease; viral disease;
 KW insect attack; nematode attack; RPE42; random oligonucleotide library;
 KW ROL; ss.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
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 FT /*tag- b
 FT /notes- "Randomised sequence"
 FT 49..66
 FT misc_feature


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FT      /*tag= C      /*tag= b
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XX      26-JUL-2001.
XX      19-JAN-2001; 2001WO-US02011.
XX      21-JAN-2000; 2000US-0177473.
XX      {PION-} PIONEER HI-BRED INT INC.
XX      Bruce WB, Niu X;
XX      WPI; 2001-442261/47.
XX      Producing tissue-preferred promoter elements constructs for regulating
XX      expression of nucleotide sequences in a plant comprises identifying and
XX      isolating tissue-preferred promoter elements .
XX      Example 1; Fig 1; 45pp; English.
XX      The sequence represents a plant root-preferred promoter element, RPE,
XX      isolated from a random oligonucleotide library (ROL). The invention
XX      concerns a method of identifying and isolating tissue-preferred promoter
XX      elements comprising the use of a mixture of random oligonucleotides,
XX      flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX      specific plant nuclear proteins, isolating the complexes and PCR
XX      amplifying the bound oligonucleotide. The method is used for isolating
XX      root-specific promoters or root-preferred promoter elements (RPE). The
XX      RPEs are useful in the genetic manipulation of a plant when operably
XX      linked to a nucleotide sequence whose expression is to be controlled to
XX      achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX      temperature, salinity, pesticide and herbicide resistance) and biotic
XX      stress (disease resistance, resistance to attack by fungi, bacteria,
XX      viruses, insects and nematodes).
XX      Sequence 66 BP; 19 A; 11 C; 21 G; 15 T; 0 other;
XX      Query Match      36.4%; Score 24; DB 22; Length 66;
XX      Best Local Similarity 100.0%; Pred. No. 0.0017;
XX      Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      43 ATTACCGTCTCAGAAATCAGCTG 66
XX      Db      43 ATTACCGTCTCAGAAATCAGCTG 66
XX      RESULT 8
XX      AAS08448
XX      ID      AAS08448 standard; DNA; 66 BP.
XX      AC      AAS08448;
XX      XX      26-SEP-2001 (first entry)
XX      DE      A plant root-preferred promoter element (RPE). RPE 89.
XX      Root preferred promoter element; RPE; abiotic stress; drought;
XX      salinity; pesticide resistance; herbicide resistance; biotic stress;
XX      disease resistance; fungal disease; bacterial disease; viral disease;
XX      insect attack; nematode attack; RPE89; random oligonucleotide library;
XX      ROL; ss.
XX      Synthetic.
XX      Key      Location/Qualifiers
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XX      FT      19..48

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KW ROL: ss.
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..18 /tag= a
 FT /label= "5' flanking_sequence"
 FT misc_feature 19..47 /tag= b
 FT /label= "Randomised sequence"
 FT misc_feature 48..65 /tag= c
 FT /label= "3' flanking_sequence"
 XX
 PN W0200153502-A2.
 XX
 XX 26-JUL-2001.
 XX
 XX 19-JAN-2001: 2001W0-US02011.
 XX
 XX 21-JAN-2000: 2000US-0177473.
 XX
 XX (PION-) PIONEER HI-BRED INT INC.
 XX
 XX Bruce WB, Niu X;
 XX
 XX WPI: 2001-442261/47.

XX Producing tissue-preferred promoter elements constructs for regulating
 XX expression of nucleotide sequences in a plant comprises identifying and
 XX isolating tissue-preferred promoter elements -
 XX
 XX Example 1: Fig 1: 45pp; English.

XX The sequence represents a plant root-preferred promoter element, RPE,
 CC isolated from a random oligonucleotide library (ROL). The invention
 CC concerns a method of identifying and isolating tissue-preferred promoter
 CC elements comprising the use of a mixture of random oligonucleotides,
 CC flanked by 5' and 3' flanking sequences, which hybridise to tissue-
 CC specific plant nuclear proteins, isolating the complexes and PCR
 CC amplifying the bound oligonucleotide. The method is used for isolating
 CC tissue-specific promoters from plants, including but not limited to
 CC root-specific promoters or root-preferred promoter elements (RPE). The
 CC RPEs are useful in the genetic manipulation of a plant when operably
 CC linked to a nucleotide sequence whose expression is to be controlled to
 CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
 CC temperature, salinity, pesticide and herbicide resistance) and biotic
 CC stress (disease resistance, resistance to attack by fungi, bacteria,
 CC viruses, insects and nematodes).

XX Sequence 65 BP; 18 A; 14 C; 17 G; 16 T; 0 other;

Query Match 30.3%; Score 20; DB 22; Length 65;
 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCTGGATCCGTTCCA 20
 Db 1 TGAGATCTGGATCCGTTCCA 20

RESULT 12
 AAS08437
 ID AAS08437 standard; DNA; 62 BP.
 XX
 AC AAS08437;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE A plant root-preferred promoter element (RPE), RPE 2.
 XX
 XX Root-preferred promoter element; RPE; abiotic stress; drought;

KW salinity; pesticide resistance; herbicide resistance; biotic stress;
 KW disease resistance; fungal disease; bacterial disease; viral disease;
 KW insect attack; nematode attack; RPE2: random oligonucleotide library;
 KW ROL: ss.
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..18 /tag= a
 FT /label= "5' flanking_sequence"
 FT misc_feature 19..44 /tag= b
 FT /label= "Randomised sequence"
 FT misc_feature 45..62 /tag= c
 FT /label= "3' flanking_sequence"
 XX
 PN W0200153502-A2.
 XX
 XX 26-JUL-2001.
 XX
 XX 19-JAN-2001: 2001W0-US02011.
 XX
 XX 21-JAN-2000: 2000US-0177473.
 XX
 XX (PION-) PIONEER HI-BRED INT INC.
 XX
 XX Bruce WB, Niu X;
 XX
 XX WPI: 2001-442261/47.

XX Producing tissue-preferred promoter elements constructs for regulating
 XX expression of nucleotide sequences in a plant comprises identifying and
 XX isolating tissue-preferred promoter elements -
 XX
 XX Claim 5: Fig 1: 45pp; English.
 XX The sequence represents a plant root-preferred promoter element, RPE,
 CC isolated from a random oligonucleotide library (ROL). The invention
 CC concerns a method of identifying and isolating tissue-preferred promoter
 CC elements comprising the use of a mixture of random oligonucleotides,
 CC flanked by 5' and 3' flanking sequences, which hybridise to tissue-
 CC specific plant nuclear proteins, isolating the complexes and PCR
 CC amplifying the bound oligonucleotide. The method is used for isolating
 CC tissue-specific promoters from plants, including but not limited to
 CC root-specific promoters or root-preferred promoter elements (RPE). The
 CC RPEs are useful in the genetic manipulation of a plant when operably
 CC linked to a nucleotide sequence whose expression is to be controlled to
 CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
 CC temperature, salinity, pesticide and herbicide resistance) and biotic
 CC stress (disease resistance, resistance to attack by fungi, bacteria,
 CC viruses, insects and nematodes).

XX Sequence 62 BP; 18 A; 11 C; 18 G; 15 T; 0 other;

Query Match 28.8%; Score 19; DB 22; Length 62;
 Best Local Similarity 100.0%; Pred. No. 0.85;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATCTGGATCCGTTCCG 19
 Db 1 TGAGATCTGGATCCGTTCCG 19

RESULT 13
 AAS08449
 ID AAS08449 standard; DNA; 66 BP.
 XX
 AC AAS08449;
 XX
 DT 26-SEP-2001 (first entry)
 XX

```

DE A plant root-preferred promoter element (RPE), RPE 22.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE22: random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..18
XX /tag= a
XX /label= "5' flanking sequence"
XX 19..48
XX /tag= b
XX /note= "Randomised sequence"
XX 49..66
XX /tag= c
XX /label= "3' flanking sequence"
XX
XX W0200153502-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-US02011.
XX
XX 21-JAN-2000; 2000US-0177473.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X;
XX
XX WPI: 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements.
XX
XX Example 1; Fig 1; 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 66 BP; 19 A; 11 C; 21 G; 15 T; 0 other;
XX
XX Query Match 28.8%; Score 19; DB 22; Length 66;
XX Best local Similarity 100.0%; Pred. No. 0.84;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TGAGATCTGGATCGGTGC 19
XX
XX 1 TGAGATCTGGATCGGTGC 19
XX
XX RESULT 14
XX AA508441
XX ID AA508441 standard; DNA: 18 BP.
XX
XX AC AA508441;

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XX 26-SEP-2001 (first entry)
XX
XX A random oligonucleotide library, ROL, PCR primer n19808.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; random oligonucleotide library;
XX ROL; n19808; ss; PCR primer.
XX
XX Synthetic.
XX
XX W0200153502-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-US02011.
XX
XX 21-JAN-2000; 2000US-0177473.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X;
XX
XX WPI: 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements.
XX
XX Example 1; Page 21; 45pp; English.
XX
XX The sequence represents a PCR primer which binds to the 5' flanking
XX region of a random oligonucleotide library (ROL) construct
XX used to isolate tissue-specific promoter elements. The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 other;
XX
XX Query Match 27.3%; Score 18; DB 22; Length 18;
XX Best local Similarity 100.0%; Pred. No. 3.3;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TGAGATCTGGATCGGTTC 18
XX
XX 1 TGAGATCTGGATCGGTTC 18
XX
XX RESULT 15
XX AA508442/c
XX ID AA508442 standard; DNA: 18 BP.
XX
XX AC AA508442;
XX
XX 26-SEP-2001 (first entry)
XX
XX A random oligonucleotide library, ROL, PCR primer n19811.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX

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XX 26-JUL-2001.
XX
XX
XX 19-JAN-2001: 2001WO-US02011.
XX
XX 21-JAN-2000: 2000US-0177473.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X;
XX
XX WPI: 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements -
XX
XX Claim 5: Fig 1: 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 64 BP: 22 A; 11 C; 16 G; 15 T; 0 other;
SQ
Query Match 27.3%; Score 18; DB 22; Length 64;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAGATCTGGATCGGTC 18
DB 1 TCACAICGGATCGGTC 18
RESULT 20
AAS08436
ID AAS08436 standard; DNA: 65 BP.
XX
XX AAS08436;
XX
XX 26-SEP-2001 (first entry)
XX
XX A plant root-preferred promoter element. (RPE), RPE 60.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE60; random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..18
XX
XX
XX misc_feature /tag= a
XX
XX /label= "5'_flanking_sequence"
XX
XX /tag= b
XX
XX /note= "Randomised sequence"
XX
XX misc_feature 48..65
XX
XX /tag= c

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```

FT
XX /label= "3'_flanking_sequence"
XX
XX WO200151502-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001: 2001WO-US02011.
XX
XX 21-JAN-2000: 2000US-0177473.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X;
XX
XX WPI: 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements -
XX
XX Claim 5: Fig 1: 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 65 BP: 16 A; 14 C; 17 G; 18 T; 0 other;
SQ
Query Match 27.3%; Score 18; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAGATCTGGATCGGTC 18
DB 1 TCAGATCTGGATCGGTC 18
RESULT 21
AAS08438
ID AAS08438 standard; DNA: 65 BP.
XX
XX AAS08438;
XX
XX 26-SEP-2001 (first entry)
XX
XX A plant root-preferred promoter element (RPE), RPE 59.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE39; random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..18
XX
XX
XX misc_feature /tag= a
XX
XX /label= "5'_flanking_sequence"
XX
XX /tag= b
XX
XX /tag= c

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FT misc_feature /note= "Randomised sequence"
FT 48..65
FT /*tag= C
FT /label= "3'_flanking_sequence"
XX
PN W0200153502-A2.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US02011.
XX
PR 21-JAN-2000; 2000US-0177473.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Bruce WB, Niu X;
XX
DR WPI; 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
PT expression of nucleotide sequences in a plant comprises identifying and
PT isolating tissue-preferred promoter elements -
XX
PS Claim 5; Fig 1; 45pp; English.
XX
CC The sequence represents a plant root-preferred promoter element, RPE,
CC isolated from a random oligonucleotide library (ROL). The invention
CC concerns a method of identifying and isolating tissue-preferred promoter
CC elements comprising the use of a mixture of random oligonucleotides,
CC flanked by 5' and 3' flanking sequences, which hybridise to tissue-
CC specific plant nuclear proteins, isolating the complexes and PCR
CC amplifying the bound oligonucleotide. The method is used for isolating
CC tissue-specific promoters from plants, including but not limited to
CC root-specific promoters or root-preferred promoter elements (RPE). The
CC RPEs are useful in the genetic manipulation of a plant when operably
CC linked to a nucleotide sequence whose expression is to be controlled to
CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
CC temperature, salinity, pesticide and herbicide resistance) and biotic
CC stress (disease resistance, resistance to attack by fungi, bacteria,
CC viruses, insects and nematodes).
XX
SQ Sequence 65 BP; 19 A; 13 C; 18 G; 15 T; 0 other;
XX
Query Match 27.3%; Score 18; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGAGATCTGGATCGGTC 18
DB 1 TGAGATCTGGATCGGTC 18
RESULT 22
AAS08440
ID AAS08440 standard; DNA; 66 BP.
XX
AC AAS08440;
XX
XX 26-SEP-2001 (first entry)
XX
DE A random oligonucleotide library, ROL, sequence n19813.
XX
KW Root preferred promoter element; RPE; abiotic stress; drought;
KW salinity; pesticide resistance; herbicide resistance; biotic stress;
KW disease resistance; fungal disease; bacterial disease; viral disease;
KW insect attack; nematode attack; random oligonucleotide library;
KW ROL; n19813; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..18
FT /*tag= a

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FT misc_feature /label= "5'_flanking_sequence"
FT 19..48
FT /*tag= b
FT /note= "Randomised sequence"
FT 49..66
FT /*tag= c
FT /label= "3'_flanking_sequence"
XX
PN W0200153502-A2.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US02011.
XX
PR 21-JAN-2000; 2000US-0177473.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Bruce WB, Niu X;
XX
DR WPI; 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
PT expression of nucleotide sequences in a plant comprises identifying and
PT isolating tissue-preferred promoter elements -
XX
PS Example 1; Page 21; 45pp; English.
XX
CC The sequence represents a random oligonucleotide library (ROL) construct
CC used to isolate tissue-specific promoter elements. The invention
CC concerns a method of identifying and isolating tissue-preferred promoter
CC elements comprising the use of a mixture of random oligonucleotides,
CC flanked by 5' and 3' flanking sequences, which hybridise to tissue-
CC specific plant nuclear proteins, isolating the complexes and PCR
CC amplifying the bound oligonucleotide. The method is used for isolating
CC tissue-specific promoters from plants, including but not limited to
CC root-specific promoters or root-preferred promoter elements (RPE). The
CC RPEs are useful in the genetic manipulation of a plant when operably
CC linked to a nucleotide sequence whose expression is to be controlled to
CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
CC temperature, salinity, pesticide and herbicide resistance) and biotic
CC stress (disease resistance, resistance to attack by fungi, bacteria,
CC viruses, insects and nematodes).
XX
SQ Sequence 66 BP; 7 A; 9 C; 9 G; 11 T; 40 other;
XX
Query Match 27.3%; Score 18; DB 22; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGAGATCTGGATCGGTC 18
DB 1 TGAGATCTGGATCGGTC 18
RESULT 24
AAS08451
ID AAS08451 standard; DNA; 66 BP.
XX
AC AAS08451;
XX
XX 26-SEP-2001 (first entry)
XX
DE A plant root-preferred promoter element (RPE), RPE 71.
XX
KW Root-preferred promoter element; RPE; abiotic stress; drought;
KW salinity; pesticide resistance; herbicide resistance; biotic stress;
KW disease resistance; fungal disease; bacterial disease; viral disease;
KW insect attack; nematode attack; RPE71; random oligonucleotide library;
KW ROL; ss.
XX
OS Synthetic.
XX

```



```

FH Key Location/Qualifiers
F1 misc_feature 1..18
F2 /tag= d
F3 /label= "5'_flanking_sequence"
F4 19..48
F5 /tag= b
F6 /note= "Randomised sequence"
F7 49..66
F8 /tag= c
F9 /label= "3'_flanking_sequence"
FN W0200153502-A2.
PD 26-JUL-2001.
PP 19-JAN-2001: 2001WO-US02011.
PR 21-JAN-2000: 2000US-0177473.
PA (PION-) PIONEER HI-BRED INT INC.
PI Bruce WB, Niu X:
P1
P2 WPI: 2001-442261/47.
DR
PT Producing tissue-preferred promoter elements constructs for regulating
PT expression of nucleotide sequences in a plant comprises identifying and
PT isolating tissue-preferred promoter elements -
PS Example 1: Fig 1: 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element. REP,
XX isolated from a random oligonucleotide library (MOL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
SU Sequence 66 BP; 19 A; 12 C; 21 G; 13 T; 1 Other;
Query Match 27.38; Score 18; DB 22; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAGATCGATCGTTCG 19
Db 2 GAGATCGATCGTTCG 19

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PN W0200170955-A2.
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001: 2001WO-US09180.
XX
XX 21-MAR-2000: 2000US-191078P.
XX 23-MAY-2000: 2000US-206848P.
XX 26-MAY-2000: 2000US-207727P.
XX 27-OCT-2000: 2000US-242578P.
XX 27-NOV-2000: 2000US-253625P.
XX 22-DEC-2000: 2000US-257931P.
XX 16-FEB-2001: 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Traxwick JD, Carr GJ:
XX Yamamoto RT, Xu HH:
XX WPI: 2001-611495/70.
XX P-PSDB: AAF35993.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Claim 27: Seq ID No 7489; 51pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the
XX genes, their use in the discovery of novel antibiotics, the essential
XX genes themselves and the encoded proteins. The prokaryotes used are
XX Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX invention is also useful for the identification of potential new targets
XX for antibiotic development. The antisense nucleic acids can also be used
XX to identify proteins used in proliferation, to express these proteins,
XX and to obtain antibodies capable of binding to the expressed proteins.
XX The proteins can be used to screen compounds in rational drug discovery
XX programmes. The antisense nucleic acid sequence is also useful to screen
XX for homologous nucleic acids which are required for cell proliferation in
XX a wide variety of organisms. The present sequence encodes an
XX essential prokaryotic cellular proliferation protein.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from WIPO at
XX http://wipo.int/pub/published\_pcl\_sequences.
XX
SU Sequence 462 BP; 142 A; 78 C; 125 G; 117 T; 0 Other;
Query Match 24.28; Score 16; DB 23; Length 462;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 TAAAAAAGCGTAGAT 44
Db 192 TAAAAAAGCGTAGAT 207

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RESULT 24
AAS53852
ID AAS53852 standard; DNA: 462 BP.
XX
AC AAS53852:
XX
DT 13-FEB-2002 (first entry)
XX
DE Helicobacter pylori DNA for cellular proliferation protein #306.
XX
KW Antisense; ds: prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Helicobacter pylori.
XX

```

```

RESULT 25
AAF60852/c
ID AAF60852 standard; DNA: 1168 BP.
XX
AC AAF60852:
XX
DT 16-MAY-2001 (first entry)
XX
DE Pseudomonas sp export system associated DNA ORF11349d.
XX
KW Export system; transgenic plant; translocation; plant growth;
KW plant development; plant yield; soil quality; phytoprotection; ds.
XX
OS Pseudomonas sp.
XX

```


XX	AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides	
CC	(11), given in AAC81454 to AAC81120, from <i>Staphylococcus epidermidis</i> .	
CC	(11) and (11) can have antibacterial activity and therefore can be used	
CC	in vaccination. The nucleic acids (11) may be used to produce the	
CC	<i>S. epidermidis</i> polypeptides (11) via the production of vectors	
CC	containing them which are used to produce hosts cells which express the	
CC	polypeptides. The polypeptides (11) (and/or nucleic acids) may then be	
CC	used to vaccinate subjects and to raise antihodis against the bacteria.	
CC	The polypeptides may also be used to assay for other inhibitors of their	
CC	activity and therefore identify compounds that may be used for the	
CC	treatment of <i>S. epidermidis</i> infections, e.g. endocarditis. AAH53971 to	
CC	AAH55990 represent specifically claimed <i>S. epidermidis</i> genomic DNA	
CC	polynucleotide sequences from the present invention. AAH55091 to	
CC	AAH55098 represent oligonucleotide sequences and primers which are used	
CC	in the exemplification of the present invention.	
CC	N.B. The present invention specifically claims all the polynucleotide	
CC	sequences given in the sequence listing of the present specification,	
CC	however the sequence listing only goes up to SEQ ID NO:4454 so even	
CC	though sequences are given in the disclosure for SEQ ID NO:4465 to 4472.	
CC	no sequences are present for SEQ ID NO:4455 to 4464.	
XX		
XX	Sequence 3032 BP; 939 A; 600 C; 422 G; 1071 T; 0 other;	
XX		
XX	Query Match 24.2%; Score 16; DB 22; Length 3032;	
XX	Best Local Similarity 100.0%; Pred. No. 24;	
XX	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		
XX	29 TAAATAAGCGGTAGAT 44	
XX		
XX	3026 TAAATAAGCGGTAGAT 3011	
XX		
XX	RESULT 28	
XX	AAH53972	
XX	AAH53972 standard; DNA; 3246 BP.	
XX		
XX	AAH53972:	
XX	03-SEP-2001 (first entry)	
XX		
XX	<i>S. epidermidis</i> genomic polynucleotide sequence SEQ ID NO:3336.	
XX		
XX	<i>Staphylococcus epidermidis</i> SRI strain; infection; diagnosis;	
XX	vaccination; endocarditis; ds.	
XX		
XX	<i>Staphylococcus epidermidis</i> .	
XX		
XX	MO200134809-A2.	
XX		
XX	17-MAY-2001.	
XX		
XX	09-NOV-2000; 2000MO-US30782.	
XX		
XX	09-NOV-1999; 990US-0164258.	
XX		
XX	(GLAXO) GLAXO GROUP LTD.	
XX		
XX	Klimmely WJ;	
XX		
XX	WPI: 2001-316435/33.	
XX		
XX	Nucleic acids encoding polypeptides from <i>Staphylococcus epidermidis</i> ,	
XX	useful for vaccinating against infections, e.g. endocarditis -	
XX		
XX	Claim 8; Page 881-882; 2188pp; English.	
XX		
XX	AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides	
XX	(11), given in AAC81454 to AAC81120, from <i>Staphylococcus epidermidis</i> .	
XX	(11) and (11) can have antibacterial activity and therefore can be used	
XX	in vaccination. The nucleic acids (11) may be used to produce the	
XX	<i>S. epidermidis</i> polypeptides (11) via the production of vectors	
XX	containing them which are used to produce hosts cells which express the	

CC polypeptides. The polypeptides (I) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g., endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.

CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4474 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.

XX SQ Sequence 3246 BP; 1091 A; 533 C; 536 G; 1086 T; 0 other;

XX QY Query Match 24.2%; Score 16; pH 22; Length 3246;
XX DB Ref Local Similarity 100.0%; Prod No. 24;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 29 TAAAGGCGTAGAT 44
XX |||||||||
XX 2668 TAAAGGCGGTACAT 2683

XX DB

XX RESULT 29

XX AAH54846/c
XX ID AAH54846 standard; DNB; 4019 BP.
XX AC
XX AAH54846;
XX DT 03-SEP-2001 (first entry)

XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4210.

XX KM Staphylococcus epidermidis SR1 strain; infection; diagnosis;
XX KW vaccination; endocarditis; ds.
XX OS Staphylococcus epidermidis.
XX PN WO2001:34809-A2.
XX PD 17-MAY-2001.
XX PE 09-NOV-2000; 2000MO-US30782.
XX PR 09-NOV-1999; 99US-0164258.
XX PA (CLAX) GLAXO GROUP LTD.
XX PI Kimmery WJ;
XX DR MPI: 2001-316495/33.
XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis.
XX PT useful for vaccinating against infections, e.g. endocarditis .

XX PS Claim 8; Page 1923-1925; 2188pp; English.

XX CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AA081454 to AA063120, from staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g., endocarditis. AAH5971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to

cc AAF55098 represent oligonucleotide sequences and primers which are used
 cc in the exemplification of the present invention.
 cc M.B. The present invention specifically claims all the polynucleotide
 cc sequences given in the sequence listing of the present specification,
 cc however the sequence listing only goes up to SEQ ID NO:4454 so even
 cc though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
 cc no sequences are present for SEQ ID NO:4455 to 4464.
 xx
 SO Sequence 4019 BP; 1292 A; 738 G; 623 G; 1366 T; 0 other;
 Query Match 24.2%; Score 16; DB 22; Length 4019;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 TAAAAAGCGTACAT 44
 ID 2617 TAAAAAGCGTACAT 2602
 RESULT 40
 AB105396/c
 ID AB105396 standard: cDNA; 7345 BP.
 AC AB105396;
 XX
 XX 26 MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10670.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 XX
 XX Drosophila melanogaster.
 OS
 PN W0200171042-A2.
 XX
 XX 27-SEP-2001.
 ID
 XX
 XX 21-MAR-2001; 2001WO-0509211.
 PE
 XX 21 MAR-2000; 2000US-191647B.
 PR
 XX 11 JUL 2000; 2000US-0614150.
 PA
 XX (P3KE) PE CORP NY.
 PT
 PT Venter JC, Adams M, Li PMD, Myers EM;
 XX
 XX WPI: 2001-656860/75.
 DR P-PSDB; ABH61293.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 PT
 XX Claim 1. SEQ ID NO 10670; 21bp + Sequence listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 XX useful in developmental biology and in elucidating cell signalling and
 XX cell-cell interactions in higher eukaryotes for the development of
 XX insecticides, therapeutics and pharmaceutical drugs. The invention
 XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 XX sequences (AB16140-AB16175) and the encoded proteins
 XX (AB16177-AB16172).
 XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WPI
 XX at http://wipo.int/pub/published_pat_sequences.
 SO
 SO Sequence 7345 BP; 1957 A; 1658 G; 1667 G; 2063 T; 0 other;
 Query Match 24.2%; Score 16; DB 23; Length 7345;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GACAAAGCGTAAAA 34
 ID 6026 GACAAAGCGTAAAA 6011
 RESULT 31
 AAF22292/c
 ID AAF22292 standard: DNA; 86584 BP.
 XX
 XX AAF22292;
 AC
 XX 20-MAR-2001 (first entry)
 DE BAC containing repeats from centromeres 1-4 #15.
 KW Centromere; microsome; vector; ds.
 XX
 XX Arabidopsis thaliana.
 OS
 PN W020005325-A2.
 XX
 XX 21-SEP-2000.
 ID
 XX
 XX 17 MAR-2000; 2000WO-0507392.
 PE
 XX 18-MAR-1999; 99US-0125219.
 PR 01-APR-1999; 99US-0127409.
 PR 18-MAY-1999; 99US-0134770.
 PR 13-SEP-1999; 99US-0153584.
 PR 17-SEP-1999; 99US-0154603.
 PA
 XX (UNYCH) UNIV CHICAGO.
 XX
 XX Preuss D, Copenhaver G, Keith K;
 PT
 XX WPI: 2000-587529/55.
 DR
 XX
 XX Recombinant DNA construct comprising a plant centromere, useful for
 PT producing stably inherited microsome which can serve as vectors for
 PT the construction of transgenic plant and animal cells.
 XX
 XX Claim 102; Page 607-626; 1449pp; English.
 PS
 XX The present invention relates to a recombinant DNA construct of a plant
 CC (Arabidopsis thaliana) centromere. The constructs are useful for
 CC producing stably inherited microsome which can serve as vectors for
 CC the construction of transgenic plant and animal cells expressing
 CC selected proteins such as hormones, enzymes, interferons, clotting
 CC factors, cytokines, antibodies, and growth factors.
 CC
 XX
 SO Sequence 86584 BP; 26755 A; 16841 G; 17276 G; 25711 T; 1 other;
 Query Match 24.2%; Score 16; DB 21; Length 86584;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 ATCCGTTGACAAAC 26
 ID 61894 ATCCGTTGACAAAC 63879
 RESULT 32
 AAQ24201/c
 ID AAQ24203 standard: DNA; 36 BP.
 AC AAQ24203;
 XX
 XX 09-OCT-1992 (first entry)
 DE Transglutaminase Primer 4.
 XX
 XX BTG: acyl rearrangement; decamination; PCR; signal; ss.

XX XX Synthetic.
 XX US EP481504-A.
 XX PN 22-APR-1992.
 XX PD 18-OCT-1991; 91RP-0117813.
 XX PR 19-OCT-1990; 90JP-0282566.
 XX PA (AJIN) AJINOMOTO CO INC.
 XX PA (AMAN) AMANO PHARM KK.
 XX PI Ando K, Arafuka S, Koikeda S, Matsui H, Takagi H, Washizu K.
 XX DR WPI; 1992-133808/17.
 XX PT DNA fragment encoding trans:glutaminase - is inserted into
 PT vector, e.g. Pml1053-BTG, for protein expression
 XX PS Disclosure; Page 27; 55pp; English.
 XX CC This DNA sequence was used in conjunction with the primer sequence
 CC given in AAQ24202 to amplify a portion of the BTG gene using PCR
 CC techniques. The portion of the gene amplified contained the signal,
 CC pro and structural sequences from BTG.
 CC BTG catalyses an acyl rearrangement reaction of a gamma-carboxyamido
 CC qp. of glutamine. It introduces intra- or intermolecular formation
 CC of epsilon-(gamma-gln)-lys cross-linking when an epsilon-amino qp.
 CC of a lys residue acts as an acyl receptor. When water acts as an
 CC acyl acceptor the enzyme accelerates the conversion of Gln residues
 CC to Gln residues by deamination.
 CC The enzyme is used in the produ. of gelled foods, gelled cosmetics,
 CC yogurt, gelatin, cheese etc. It is also used in the produ. of
 CC thermally stable materials such as microcapsules and carriers of
 CC immobilized enzymes. The DNA sequence given allows the produ. of
 CC BTG efficiently and in large quantity.
 XX SO Sequence 36 BP; 7 A; 15 C; 7 G; 7 T; 0 other;
 Query Match 22.7%; Score 15; DB 13; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAGATCTGGATCCG 15
 DB 16 TGAATCTGGATCCG 2
 RESULT 33
 AAD03192/c
 ID AAD03192 standard; DNA: 44 BP.
 XX AC AAD03192:
 XX 13-JUN-2001 (first entry)
 XX DE PCR primer #2 used to isolate Zea mays 700266438 clone promoter cDNA.
 XX KW Corn; 700266438 clone; promoter; morphology; physiology; growth; seed;
 KW development; nutritional enhancement; disease resistance; plant embryo;
 KW environmental tolerance; chemical tolerance; pest resistance;
 KW genetic engineering; gene expression; PCR primer; ss.
 XX OS Zea mays.
 XX FN M0200116407-A2.
 XX PD 08-MAR-2001.
 XX PF 30-AUG-2000; 2000MO-US23824.

PR 01-SEP-1999; 990US-0151892.
 XX PA (RENE-) RENNESSEN LLC.
 XX PI Conner IW, Tzafirir I;
 XX DR WPI; 2001-244405/25.
 XX PT New plant regulatory DNA sequences, useful for selectively controlling
 PT gene expression and for modifying plants through genetic engineering to
 PT have the desired morphology, physiology, growth or nutritional
 XX PS enhancement -
 XX PS Example 3; Page 72; 80pp; English.
 XX CC The present invention relates to nucleic acid sequences for regulating
 CC gene expression in plants. The promoter nucleic acid molecules are useful
 CC for controlling gene expression in plants. The promoter DNA sequences are
 CC also useful for expression of transgene products in plant embryos and
 CC plant seeds. The plant promoters are useful for modifying plants through
 CC genetic engineering to have the desired characteristics associated with
 CC plant morphology, physiology, growth and development yield, nutritional
 CC enhancement, diseases or pest resistance, or environmental or chemical
 CC tolerance.
 CC The present sequence is a PCR primer used along with an adaptor primer 2
 CC (AP2) (AAD03171) in the nested PCR reaction to isolate Zea mays
 CC 700266438 clone promoter cDNA.
 XX SO Sequence 44 BP; 9 A; 18 C; 6 G; 11 T; 0 other;
 Query Match 22.7%; Score 15; DB 22; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAGATCTGGATCCG 15
 DB 17 TGAATCTGGATCCG 3
 RESULT 34
 AAN60630
 ID AAN60630 standard; DNA: 478 BP.
 XX AC AAN60630:
 XX 17-JUN-1991 (first entry)
 XX DE beta-urogastrone - beta-lactamase fusion gene from pUG2301.
 XX KW Beta-urogastrone gene; hormone; salivary gland; ulcers; wounds;
 KW fusion protein; beta-lactamase; ss.
 XX OS Synthetic.
 XX FH Key
 FH CDS 1..357 location/Qualifiers
 FT /tag= a
 FT /product= fusion_protein
 FT 1..188
 FT /tag= b
 FT /product= beta_lactamase
 FT 189..198
 FT /tag= c
 FT /label= adaptor
 FT 199..357
 FT CDS /tag= d
 FT /product= beta-urogastrone
 XX PN DE3523634-A.
 XX PD 09-JAN-1986.
 XX PF 02-JUL-1985; 85DE-3523634.

```

XX 02-JUL-1984: H4JP-0147691.
XX
XX (PART-) EARTH CHEMICAL CO.,
XX
XX Aoki S, Ohgaki H, Horinaka A, Hiramatsu H, Koumoto S, Nishimura A;
XX Matsushiro S;
XX WPI: 1986-01501/03.
XX
XX P-PSDB: AAP60626.
XX
XX New gene for expression of beta-urogastrone (its derivative, plasmids)
XX and transformed cells contg. it.
XX
XX Disclosure: Page 55-56; 92pp; German.
XX
XX This sequence includes the sequence of claim 1 (bases 199-357)
XX modified by restriction sites for coupling to the beta-lactamase
XX gene and insertion into plasmids. Beta-urogastrone can then
XX easily recovered from the fusion protein expressed by transformants.
XX The fusion protein is less easily degraded by proteases and so
XX protects beta-urogastrone and beta-lactamase collect in the periplasm
XX of E.coli. It is therefore easy to collect and purify the product.
XX Beta-urogastrone is the hormone of the salivary glands which suppresses
XX stomach acid secretion and promotes cell growth, so is useful for
XX treating ulcers and wounds. Previously the product was obtd. only
XX in small ants, from human urine.
XX See also AAM60626, and 30-32.
XX
XX Sequence 478 BP: 111 A; 102 C; 125 G; 140 T; 0 other;
XX
XX Query Match 22.7%; Score 15; DB 7; Length 478;
XX Best Local Similarity 100.0%; Pred. No. 99;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ACATCTGATCGCTT 17
XX |||||||
XX 467 ACATCTGATCGCTT 481
XX
XX RESULT 35
XX ID AAZ91620 standard; DNA: 533 BP.
XX
XX AAZ91620;
XX
XX 17 MAY-2000 (first entry)
XX
XX E.coli promoter region flanking sequence, DDP2087 upper.
XX
XX Promoter region; regulatory region identification; flanking sequence;
XX cellular insult, luciferase; thermostable lux gene complex;
XX LUXCABE gene complex; crop protection chemical;
XX stress responsive regulatory region; ss.
XX
XX Escherichia coli.
XX
XX US6025141-A.
XX
XX 15-FEB-2000.
XX
XX 23-OCT-1996; 960S-075545.
XX
XX 23-OCT-1996; 960S-075545.
XX
XX (DDPO) DU POINT DE NEMOURS & CO E.L.
XX
XX LATOSSA RA, Van Dyk TK;
XX
XX WPI: 2000-181802/16.
XX
XX Identification of regulatory regions modulated by a cellular insult,
XX PT such as crop protection chemicals -
XX

```

```

XX Example: Column 29-30; 31pp; English.
XX
XX This sequence is a flanking sequence for an E. coli promoter region.
XX The invention relates to a method for identifying regulatory regions
XX modulated by a cellular insult, comprising: (a) creating a library of
XX gene fusions of genomic DNA fused to a promoterless, luminescent reporter
XX gene complex selected from a gene complex encoding luciferase from
XX Renella species; a thermostable lux gene complex, and a LUXCABE gene
XX complex in enteric bacteria to create fusion-containing strains;
XX (b) culturing individual gene fusion-containing strains in liquid media;
XX (c) contacting the fusion-containing strains at a particular growth
XX phase with a cellular insult; and (d) analysing the fusion-containing
XX strain for a change in luminescence, the change in luminescence
XX indicating that the fusion-containing strain includes a regulatory region
XX modulated by the cellular insult. The method is useful for identifying
XX regulatory regions affected by cellular stress such as that created by
XX crop protection chemicals. The method can detect promoters or stress
XX responsive regulatory regions undetectable by prior art methods.
XX
XX Sequence 533 BP: 166 A; 94 C; 140 G; 133 T; 0 other;
XX
XX Query Match 22.7%; Score 15; DB 21; Length 533;
XX Best Local Similarity 100.0%; Pred. No. 99;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 22 AAACGGTAAAAAG 36
XX |||||||
XX 72 AAACGGTAAAAAG 86
XX
XX RESULT 36
XX ID AAF55139 standard; DNA: 533 BP.
XX
XX AAF55139;
XX
XX 29-MAY-2001 (first entry)
XX
XX Sulfometuron methyl-responsive regulatory region binding sequence.
XX
XX Escherichia coli; regulatory region; cellular insult; crop protection;
XX sulfometuron methyl-responsive regulatory region; cellular stress;
XX herbicide; environmental pollutant; heavy metal; oxidative damage;
XX anaerobiosis; ss.
XX
XX Unidentified.
XX
XX US6194159-B1.
XX
XX 27-FEB-2001.
XX
XX 24-NOV-1999; 990S-0449083.
XX
XX 23-OCT-1996; 960S-075545.
XX
XX (DDPO) DU POINT DE NEMOURS & CO E.L.
XX
XX LATOSSA RA, Van Dyk TK;
XX
XX WPI: 2001-217925/22.
XX
XX Novel Escherichia coli genome segment, useful for detecting bacterial
XX regulatory elements responsive to variety of cellular stresses.
XX PT consists of sulfometuron methyl-responsive regulatory region -
XX
XX Claim 13; Column 29-30; 35pp; English.
XX
XX The specification describes an Escherichia coli regulatory region
XX modulated by a cellular insult. The regulatory region is preferably a
XX sulfometuron methyl (SM)-responsive regulatory region, preferably
XX bound by the sequences given in AAF55139-40. The recombinant E. coli
XX are useful for detecting crop protection chemicals and for detecting
XX

```

```
CC bacterial regulatory elements responsive to a variety of cellular
CC stresses (produced by cellular insults) such as herbicides,
CC environmental pollutants, heavy metals, changes in temperature, changes
CC in pH, agents producing oxidative damage, insults causing DNA damage,
CC insults causing aneuploidy, and biological insults such as the
CC pathogenic life forms.
XX
SU Sequence 533 BP; 166 A; 94 C; 140 G; 133 T; 0 other:
XX
Query Match 22.78; Score 15; DH 22; Length 533;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
YY 22 AAACCGTAAAAAG 36
XXXXXXXXXXXXXXXXXXXX
DB 72 AAACCGTAAAAAG 86
XXXXXXXXXXXXXXXXXXXX
RESULT 37
AAN60632
ID AAN60632 standard; DNA: 539 BP.
XX
AC AAN60632;
XX
DE 17-JUN-1991 (first entry)
XX
DE Beta-urogastrone - beta-lactamase fusion gene from pUG2701.
XX
KM Beta-urogastrone gene; hormone; salivary gland; ulcers; wounds;
KM fusion protein; beta-lactamase; ss.
XX
OS Synthetic.
XX
EH Key Location/Qualifiers
FT CDS 1..477
FT /tag= a
FT /product= fusion_protein
FT CDS 1..307
FT /tag= b
FT /product= beta-lactamase
FT misc_RNA 308..318
FT /tag= c
FT /label= adaptor
FT CDS 319..477
FT /tag= d
FT /product= beta-urogastrone
XX
PN DE3523634-A.
XX
PD 09-JAN-1986.
XX
PE 02-JUL-1985; 85DB-3523634.
XX
PR 02-JUL-1984; 84JP-0137691.
XX
PA (EART-) EARTH CHEMICAL CO.
XX
PI Aoki S, Ohgai H, Horioka A, Hiramatsu H, Koumoto S, Nishimura A;
PI Matsushiro S;
XX
DR WPI: 1986-015031/03.
DR P-PSDB: AAP60628.
XX
PT New gene for expression of beta-urogastrone - its derivs., plasmid(s)
PT and transformed cells contg. it.
XX
PS Disclosure; Page 59-61; 92pp; German.
XX
CC This sequence includes the sequence of claim 1 (bases 319-477)
CC modified by restriction sites for coupling to the beta-lactamase
CC gene and insertion into plasmids. Beta-urogastrone can then
CC easily recovered from the fusion protein expressed by transformants.
CC The fusion protein is less easily degraded by proteases and so
```

```
CC protects beta-urogastrone and beta-lactamase collectis in the periplasm
CC of E.coli. It is therefore easy to collect and purify the product.
CC Beta-urogastrone is the hormone of the salivary glands which suppresses
CC stomach acid secretion and promotes cell growth, so is useful for
CC treating ulcers and wounds. Previously the product was obt'd. only
CC in small amts. from human urine.
CC See also AAN60628, and 30-32.
XX
SU Sequence 539 BP; 130 A; 116 C; 137 G; 156 T; 0 other:
XX
Query Match 22.78; Score 15; DH 7; Length 539;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
YY 3 AGATCTGATTCGCT 17
XXXXXXXXXXXXXXXXXXXX
DB 487 AGATCTGATTCGCT 501
XXXXXXXXXXXXXXXXXXXX
RESULT 38
AAN60631
ID AAN60631 standard; DNA: 654 BP.
XX
AC AAN60631;
XX
DE 17-JUN-1991 (first entry)
XX
DE Beta-urogastrone - beta-lactamase fusion gene from pUG2101.
XX
KM Beta-urogastrone gene; hormone; salivary gland; ulcers; wounds;
KM fusion protein; beta-lactamase; ss.
XX
OS Synthetic.
XX
EH Key Location/Qualifiers
FT CDS 1..588
FT /tag= a
FT /product= fusion_protein
FT CDS 1..419
FT /tag= b
FT /product= beta-lactamase
FT misc_RNA 420..429
FT /tag= c
FT /label= adaptor
FT CDS 430..588
FT /tag= d
FT /product= beta-urogastrone
XX
PN DE3523634-A.
XX
PD 09-JAN-1986.
XX
PE 02-JUL-1985; 85DB-3523634.
XX
PR 02-JUL-1984; 84JP-0137691.
XX
PA (EART-) EARTH CHEMICAL CO.
XX
PI Aoki S, Ohgai H, Horioka A, Hiramatsu H, Koumoto S, Nishimura A;
PI Matsushiro S;
XX
DR WPI: 1986-015031/03.
DR P-PSDB: AAP60627.
XX
PT New gene for expression of beta-urogastrone - its derivs., plasmid(s)
PT and transformed cells contg. it.
XX
PS Disclosure; Page 56-59; 92pp; German.
XX
CC This sequence includes the sequence of claim 1 (bases 430-588)
CC modified by restriction sites for coupling to the beta-lactamase
CC gene and insertion into plasmids. Beta-urogastrone can then
CC easily recovered from the fusion protein expressed by transformants.
```

CC The fusion protein is less easily degraded by proteases and so
 CC protects beta-urogastrone and beta-lactamase collects in the periplasm
 CC of E. coli. It is therefore easy to collect and purify the product.
 CC beta-urogastrone is the hormone of the salivary glands which suppresses
 CC stomach acid secretion and promotes cell growth, so is useful for
 CC treating ulcers and wounds. Previously the product was obtd. only
 CC in small amts. from human urine.
 CC See also AAN6062H, and 30-42.
 CC
 XX
 SQ Sequence 654 BP; 166 A; 142 C; 163 G; 183 T; 0 other;
 Query Match 22.7%; Score 15; DB 7; Length 654;
 Best Local Similarity 100.0%; Prod. No. 97;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 AGATCTGCATCGCTT 17
 ID 598 AGATCTGCATCGCTT 612
 RESULT 39
 AA194990
 ID AA194990 standard; cDNA; 847 BP.
 XX
 AC AA194990;
 XX
 DT 13 NOV-2001 (first entry)
 XX
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 65.
 XX
 KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TRKA; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200166719-A1.
 XX
 ID 13 SEP-2001.
 XX
 PE 02-MAR-2001; 2001WO-JP01629.
 XX
 PR 07-MAR-2000; 2000JP-0159195.
 XX
 PA (CHIB-) CHIBA PREFECTURE.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Nakagawara A;
 XX
 DK WP1: 2001-565584/63.
 XX
 PT Nucleic acids originating in gene expressed in human neuroblastoma,
 PT useful as probe or primer in diagnosing prognosis of human
 PT neuroblastoma, malignancy and susceptibility indicator or tumour marker
 PT for anti-cancer agents
 XX
 PS Claim 1; Page 84; 297pp; Japanese.
 XX
 CC The invention relates to novel genes (AA194926-AA197963) expressed in
 CC human neuroblastoma. The nucleic acids are applicable as a probe or
 CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and
 CC susceptibility indicators or tumour markers for anti-cancer agents. The
 CC gene information for diagnosing prognosis is related to factors similar
 CC to that for N-myc and TRKA genes.
 CC
 XX
 SQ Sequence 847 BP; 216 A; 238 C; 184 G; 186 T; 24 other;
 Query Match 22.7%; Score 15; DB 22; Length 847;
 Best Local Similarity 100.0%; Prod. No. 95;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GAGATCTGCATCGCT 16
 ID 212 GAGATCTGCATCGCT 226

RESULT 40
 AA194316
 ID AA194316 standard; cDNA; 883 BP.
 XX
 AC AA194316;
 XX
 DT 13 NOV-2001 (first entry)
 XX
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 191.
 XX
 KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TRKA; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200166719-A1.
 XX
 ID 13-SEP-2001.
 XX
 PE 02-MAR-2001; 2001WO-JP01629.
 XX
 PR 07-MAR-2000; 2000JP-0159195.
 XX
 PA (CHIB-) CHIBA PREFECTURE.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX
 PI Nakagawara A;
 XX
 DR WP1: 2001-565584/63.
 XX
 PT Nucleic acids originating in gene expressed in human neuroblastoma,
 PT useful as probe or primer in diagnosing prognosis of human
 PT neuroblastoma, malignancy and susceptibility indicator or tumour marker
 PT for anti-cancer agents
 XX
 PS Claim 1; Page 330; 297pp; Japanese.
 XX
 CC The invention relates to novel genes (AA194926-AA197963) expressed in
 CC human neuroblastoma. The nucleic acids are applicable as a probe or
 CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and
 CC susceptibility indicators or tumour markers for anti-cancer agents. The
 CC gene information for diagnosing prognosis is related to factors similar
 CC to that for N-myc and TRKA genes.
 CC
 XX
 SQ Sequence 883 BP; 235 A; 232 C; 187 G; 178 T; 51 other;
 Query Match 22.7%; Score 15; DB 22; Length 883;
 Best Local Similarity 100.0%; Prod. No. 94;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GAGATCTGCATCGCT 16
 ID 189 GAGATCTGCATCGCT 203
 RESULT 41
 AA254037c
 ID AA254037 standard; DNA; 969 BP.
 XX
 AC AA254037;
 XX
 DT 21 MAR-2000 (first entry)
 XX
 DE Neisseria meningitidis ORF 629 partial DNA sequence SEQ ID NO:2023.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
 KW antibacterial; gene therapy; ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN W09957280-A2.

PD 11-NOV-1999.
 XX 30-APR-1999; 99MO-US09346.
 XX 01-MAY-1998; 98US-0083758.
 PR 31-JUL-1998; 98US-0094869.
 PR 02-SEP-1998; 98US-0094894.
 PR 02-SEP-1998; 98US-0094962.
 PR 09-OCT-1998; 98US-0103749.
 PR 09-OCT-1998; 98US-0103794.
 PR 09-OCT-1998; 98US-0103796.
 PR 25-FEB-1999; 99US-0121528.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Fraser C, Galeotti C, Grandi G, Hickey F, Masigrani V, Mora M;
 PI Petersen J, Pizsa M, Rappulli R, Ratti G, Scalato E, Scarselli M;
 PI Tectelin H, Venter JC;
 XX
 DR WPI: 2000-062150/05.
 DR P-PSDB: AAY75275.
 XX
 PI Novel Neisserial polypeptides predicted to be useful antigens for
 PI vaccines and diagnostics
 XX
 PS Claim 7; Page 1005; 1453pp; English.
 XX
 CC AA253015 to AA254546, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel Neisseria meningitis and N. gonorrhoea polynucleotides
 CC and polypeptides. AA254577 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenetic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
 CC presence of Neisseria bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.
 XX
 SO Sequence 969 BP; 136 A; 236 C; 317 G; 280 T; 0 other;
 Query Match 22.7%; Score 15; DB 21; Length 969;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 CTTGCACAAAACGCT 29
 Db 244 CTTGCACAAAACGCT 230
 RESULT 42
 AAF94369/c
 ID AAF94369 standard; DNA: 1104 BP.
 XX
 AC AAF94369;
 XX
 DT 04-JUN-2001 (first entry)
 XX
 DE Haemophilus influenzae essential bacterial gene SPO ID NO:49.
 XX
 KW Haemophilus influenzae: essential bacterial gene; identification;
 KW otitis media; meningitis; upper respiratory tract infection;
 KW infection; antimicrobial; ds.
 XX
 OS Haemophilus influenzae.
 XX
 PN W02001103-A2.
 XX
 PD 15-FEB-2001.
 XX

PF 03-AUG-2000; 200CWO-US21176.
 XX
 PR 04-AUG-1999; 99US-0368382.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Chovan LE, Hessler PE, Reich KA;
 XX
 DR WPI: 2001-147511/15.
 DR P-PSDB: AAB88516.
 XX
 PI Essential bacterial genes from Haemophilus influenzae and methods for
 PI identifying 'essential' genes that may be potential therapeutic targets
 PT
 PS Claim 2; Page 90-91; 185pp; English.
 XX
 CC AAF94345 to AAF94409 represent essential bacterial genes from
 CC Haemophilus influenzae, which encode the proteins given in AAB88492 to
 CC AAB88556. The present invention also describes methods for identifying
 CC essential bacterial genes (i.e. those essential to the survival of a
 CC bacterium) using a transposition system. The methods are used to
 CC identify essential genes from bacteria, especially H. influenzae (which
 CC causes otitis media, meningitis and upper respiratory tract infections)
 CC which may be used as targets for potential antimicrobial agents.
 CC AAF94410 to AAF94416 represent PCR primers used in the exemplification
 CC of the present invention.
 XX
 SO Sequence 1104 BP; 347 A; 195 C; 219 G; 343 T; 0 other;
 Query Match 22.7%; Score 15; DB 22; Length 1104;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 31 AAAAAGCGGTACATT 45
 Db 729 AAAAAGCGGTACATT 715
 RESULT 43
 AAX14265
 ID AAX14265 standard; DNA: 1170 BP.
 XX
 AC AAX14265;
 XX
 DT 31-MAR-1999 (first entry)
 XX
 DE H. pylori GHP0 1564 gene.
 XX
 KW GHP0 protein; Helicobacter infection; gastroduodenal disease; gastritis;
 KW peptic ulcer disease; ss.
 XX
 OS Helicobacter pylori.
 XX
 FH Key Location/Qualifiers
 FT CDS 97..1122
 FT /1122
 FT /1122
 FT /1122
 XX
 PN W09843478-A1.
 XX
 PD 08-OCT-1998.
 XX
 PE 01-APR-1998; 98MO-US06371.
 XX
 PR 29-JUL-1997; 97US-0902615.
 PR 01-APR-1997; 97US-0835457.
 PR 24-JUN-1997; 97US-0881227.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
 XX
 PI Al-Garawi A, Kleantrous H, Miller C, Cohen RP, Tomb J;
 XX

DR WPI: 1998-542293/46.
DR P-PSDB: AAW98546.
XX
XX New isolated helicobacter polynucleotides - used to develop products
for the diagnosis, prevention and treatment of helicobacter
infections and gastrointestinal diseases
XX
XX Claim 1: Page 1053-1055; 2054pp; English.
XX This sequence represents a polynucleotide of the invention. It was
isolated from helicobacter pylori and encodes a H-pylori GfxO protein.
CC The polypeptides can be used for preventing or treating helicobacter
infections, and gastroduodenal diseases associated with these
infections, including acute, chronic, and atrophic gastritis, and peptic
ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used
CC for the production of antibodies. The products can also be used for
detection and diagnosis.
XX
XX Sequence 1170 BP; 380 A; 180 C; 272 G; 338 T; 0 other:
Query Match 22.7%; Score 15; BH 19; length 1170;
Best Local Similarity 100.0%; Prvd. No. 92;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GY 29 TAAAGAGGCTGACA 43
DB #55 TAAAGAGGCTGACA 869
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RESULTS 44
AB019747 standard; DNA; 1457 BP.
XX
XX AB019747:
AC
XX
XX 23-JAN-2002 (first entry)
XX
XX Human nervous system related polynucleotide SEQ ID NO 12078.
DB
XX
XX Human; neoplastic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnervary;
antiparkinsonian; antistroke; antianemic; antitubercular; cancer;
KW antihematuric; hepatotropic; cerebroprotective; antiinflammatory;
KW antilepteric; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; neurotropic; gene therapy; vaccine; dis-
XX
XX Homo sapiens.
OS
XX
XX W0200159063-A2.
XX
XX 16-AUG-2001.
XX
XX 17-JAN-2001; 2001MO-US01334.
XX
XX 31-JAN-2000; 2000US-0174065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-MAR-2000; 2000US-0198124.
XX 19-MAR-2000; 2000US-0200515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225216.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227094.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 05-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235844.
PR 27-SEP-2000; 2000US-0235844.
PR 27-SEP-2000; 2000US-0235845.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0236945.
PR 13-OCT-2000; 2000US-0236947.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0246417.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.

CC	PR	08-NIV-2000;	2000US-0246477.
CC	PR	08-NIV-2000;	2000US-0246478.
CC	PR	08-NIV-2000;	2000US-0246523.
CC	PR	08-NIV-2000;	2000US-0246524.
CC	PR	08-NIV-2000;	2000US-0246525.
CC	PR	08-NIV-2000;	2000US-0246526.
CC	PR	08-NIV-2000;	2000US-0246527.
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CC	PR	08-NIV-2000;	2000US-0246532.
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CC	PR	08-NIV-2000;	2000US-0246610.
CC	PR	08-NIV-2000;	2000US-0246613.
CC	PR	17-NIV-2000;	2000US-0249207.
CC	PR	17-NIV-2000;	2000US-0249208.
CC	PR	17-NIV-2000;	2000US-0249209.
CC	PR	17-NIV-2000;	2000US-0249210.
CC	PR	17-NIV-2000;	2000US-0249211.
CC	PR	17-NIV-2000;	2000US-0249212.
CC	PR	17-NIV-2000;	2000US-0249213.
CC	PR	17-NIV-2000;	2000US-0249214.
CC	PR	17-NIV-2000;	2000US-0249215.
CC	PR	17-NIV-2000;	2000US-0249264.
CC	PR	17-NIV-2000;	2000US-0249265.
CC	PR	17-NIV-2000;	2000US-0249297.
CC	PR	17-NIV-2000;	2000US-0249299.
CC	PR	17-NIV-2000;	2000US-0249300.
CC	PR	01-DEC-2000;	2000US-0250391.
CC	PR	01-DEC-2000;	2000US-0250390.
CC	PR	05-DEC-2000;	2000US-0250390.
CC	PR	05-DEC-2000;	2000US-0251988.
CC	PR	05-DEC-2000;	2000US-0256719.
CC	PR	08-DEC-2000;	2000US-0251479.
CC	PR	08-DEC-2000;	2000US-0251856.
CC	PR	08-DEC-2000;	2000US-0251869.
CC	PR	08-DEC-2000;	2000US-0251889.
CC	PR	08-DEC-2000;	2000US-0251990.
CC	PR	11-DEC-2000;	2000US-0254097.
CC	PR	05-JAN-2001;	2001US-0259678.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	PI	Rosen CA, Harash SC, Rubin SM:	
XX	PT	WPI; 2001-541565/60.	
XX	XX	Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases - disclosure; SEQ ID NO 12078; 1701pp + Sequence Listing; English.	
CC	CC	The invention relates to novel genes (ABAI1004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.	

```

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at http://wipo.int/pub/published\_pct\_sequences.
CC
XX
XX Sequence 1457 BP; 383 A; 345 C; 263 G; 466 T; 0 other;
SO
  Query Match      22.7%; Score 15; DB 22; Length 1457;
  Best Local Similarity 100.0%; Pred. No. 90;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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  DB      731 AAAAGCGGATTA 745
  RESULT 45
  ABL02975
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  AC
  AG ABL02975;
  AT
  CT 26-MAR-2002 (first entry)
  DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3407.
  EE
  FF Drosophila; developmental biology; cell signalling; insecticide;
  GW pharmaceutical; gene; ss.
  XX
  OS Drosophila melanogaster.
  PN WO200171042-A2.
  PR
  PD 27-SEP-2001.
  PE
  PF 23-MAR-2001; 2001WO-US09231.
  PG
  PH 23-MAR-2000; 2000US-191637P.
  PI 11-JUL-2000; 2000US-0614150.
  PP
  PQ (PEKE ) PE CORP NY.
  PR
  PS
  PT Venter JC, Adams M, Li PMD, Myers EW;
  PU
  PZ WIPI: 2001-656860/75.
  DR P-PSDB; ABH58872.
  XX
  XX New isolated nucleic acid detection reagent for detecting 1000 or more
  PT genes from Drosophila and for elucidating cell signalling and cell-cell
  PT interactions -
  PS
  PS Claim 1; SEQ ID NO 3407; 21pp + Sequence listing; English.
  XX
  XX The invention relates to an isolated nucleic acid detection reagent
  CC capable of detecting 1000 or more genes from Drosophila. The invention is
  CC useful in developmental biology and in elucidating cell signalling and
  CC cell-cell interactions in higher eukaryotes for the development of
  CC insecticides, therapeutics and pharmaceutical drugs. The invention
  CC discloses genomic DNA sequences (ABE16176-ABE140511), expressed DNA
  CC sequences (ABH10840-ABH16175) and the encoded proteins
  CC (AAB57737-ABH72072).
  CC The sequence data for this patent did not form part of the printed
  CC specification, but was obtained in electronic format directly from WIPO
  CC at http://wipo.int/pub/published\_pct\_sequences.
  CC
  SO Sequence 1550 BP; 380 A; 406 C; 408 G; 356 T; 0 other;
  OY      20 ACAAAACGGTAAAA 34
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  DB      175 ACAAAACGGTAAAA 189

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Search completed: November 5, 2002, 08:24:50
Job Time : 123.815 Secs

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OM nucleic - nucleic search, using sw model

Run on: November 5, 2002, 07:02:08 : Search time 760.981 Seconds

(Without alignments)
1126.196 Million cells updates/sec

Title: US-09-766-113-2

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Total number of hits satisfying chosen parameters: 27472414

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Post-processing: Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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3	17	25.8	568	10	B1008710	B1008710	B1008710	B1008710
4	17	25.8	630	10	B1008710	B1008710	B1008710	B1008710
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21	16	24.2	516	10	B1607662	B1607662	B1607662	B1607662
22	16	24.2	532	10	B1584222	B1584222	B1584222	B1584222
23	16	24.2	540	9	B1584222	B1584222	B1584222	B1584222
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27	16	24.2	574	12	T4558110	T4558110	T4558110	T4558110
28	16	24.2	580	10	B1585318	B1585318	B1585318	B1585318
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32	16	24.2	617	10	B1237091	B1237091	B1237091	B1237091
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34	16	24.2	635	12	A0950782	A0950782	A0950782	A0950782
35	16	24.2	647	10	B1624045	B1624045	B1624045	B1624045
36	16	24.2	649	9	AA202447	AA202447	AA202447	AA202447
37	16	24.2	653	10	B1229347	B1229347	B1229347	B1229347
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39	16	24.2	660	12	AZ573452	AZ573452	AZ573452	AZ573452
40	16	24.2	668	10	B1234820	B1234820	B1234820	B1234820
41	16	24.2	672	12	AZ572058	AZ572058	AZ572058	AZ572058
42	16	24.2	673	10	B1621542	B1621542	B1621542	B1621542
43	16	24.2	679	12	AZ569442	AZ569442	AZ569442	AZ569442
44	16	24.2	681	10	B1582214	B1582214	B1582214	B1582214
45	16	24.2	690	9	BH412863	BH412863	BH412863	BH412863
	16	24.2	694	10	B1954699	B1954699	B1954699	B1954699

ALIGNMENTS

RESULT 1
A1755421/c
DEFINITION
LOCUS
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 456)
Liberator P., Diaz C., Tang K., Marra M., Hillier L., Kucaba T.,
Martin J., Wyllie T., Underwood K., Steptoe M., Theisinger R., Allen
M., Bowers Y., Person R., Swaller T., Gibbons M., Pape D., Harvey
N., Schurk R., Riller E., Kohn S., Florence N., Shim T., Jackson
Y., Cardenas M., McCann R., Waterson R., Wilson R. and Sibley D.
WashU-Merck Eimeria tenella project
Unpublished (1999)
Contact: David Sibley, Ph.D.
WashU-Merck Eimeria tenella project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est.watson.wustl.edu
Contact David Sibley (toxepest@wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40bp from GlcC
High quality sequence stop: 418.
Location/Qualifiers
1..456
/organism="Eimeria tenella"
/strain="LS18"
/db_xref="taxon:5802"
/clone_lib="Eimeria S5-2 sporozoite stage"
/dev_stage="Sporozoite"
/lab_host="SOLR E. coli"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI

COMMENT

TITLE

JOURNAL

FEATURES
Source

1..456
/organism="Eimeria tenella"
/strain="LS18"
/db_xref="taxon:5802"
/clone_lib="Eimeria S5-2 sporozoite stage"
/dev_stage="Sporozoite"
/lab_host="SOLR E. coli"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI

: Sporozoites were obtained from in vitro sporulated and excysted oocysts of *E. tenella* grown in chickens. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size-selected on Sephacryl S500. cDNAs were digested with EcoRI/XhoI and cloned into lambda Zap II (Stratagene). Clones were converted to phagemids by mass excision using Exassist helper phage and SOL8 cells (Stratagene).

BASE COUNT 106 a 122 c 114 g 114 t
Insert sizes range from 1.2-2.9 kb.

Query Match 25.8% Score 17: DB 9: Length 456;
Best Local Similarity 100.0% Pred. No. 39;

Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 9 GATCTGCTTACAAAA 25
|||||
Db 43 GATTCGCTTACAAAA 17

RESULT 2
LOCUS BE775681
DEFINITION MY-05-E-11 *Plutostansky phycophthora infestans* cDNA, mRNA sequence.
ACCESSION BE775681
VERSION BE775681.1 GI:10229336
KEYWORDS EST.
SOURCE potato late blight agent.
ORGANISM *Phycophthora infestans*
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE 1 (bases 1 to 559)
Kamoun, S., Hrabov, P.T., Sobral, R.M.S., Nuss, P. and Govers, F.
Initial assessment of gene diversity for the complete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
CONTACT: Govers, F.
Laboratory of Phytopathology
Wageningen University
Rimshoven 9, P.O. Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francoise.Govers@medew.tyo.wau.nl
LOCATION/Qualifiers
1..559

FEATURES
SOURCE

/organism "*Phycophthora infestans*"
/strain "DBR7602, Al mating type"
/db_xref "taxon:4787"
/clone_1db "Plutostansky"
/dev_stage "4 week old vegetative, non-sporulating
mycelium in synthetic medium"
/lab_host "E. coli, strain DH5-alpha"
/note "vector: pSPOR1; site_1: SalI; site_2: NotI. Total
RNA was isolated from mycelium of *P. infestans* DBR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."

BASE COUNT 123 a 160 c 145 g 128 t
ORIGIN

Query Match 25.8% Score 17: DB 10: Length 559;
Best Local Similarity 100.0% Pred. No. 38;
Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GATATTCGATCGCTTC 18
|||||
Db 225 GATATTCGATCGCTTC 209

RESULT 3
BJ008710 568 bp mRNA linear EST 05-DEC-2001
LOCUS BJ008710 MF01SSA cDNA *Oryzias latipes* cDNA clone MF01SSA1.2011 5',
DEFINITION mRNA sequence.
ACCESSION BJ008710
VERSION BJ008710.1 GI:17356542
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM *Oryzias latipes*
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; *Oryzias*.
REFERENCE 1 (bases 1 to 568)
Kohara, Y., Shin-I, T., Kimura, T., Narita, T., Jinbo, T. and Takeda, H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
CONTACT: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genres.nig.ac.jp
LOCATION/Qualifiers
1..568

FEATURES
SOURCE

/organism "*Oryzias latipes*"
/strain "Hd-TK"
/db_xref "taxon:8090"
/clone_1db "MF01SSA1.2011"
/clone_1db "MF01SSA cDNA"
/sex "mixture of female and male"
/issue_type "whole embryo"
/dev_stage "segmentation stage 20 - 25"

BASE COUNT 117 a 155 c 195 g 101 t
ORIGIN

Query Match 25.8% Score 17: DB 10: Length 568;
Best Local Similarity 100.0% Pred. No. 38;
Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 ACATCGATCGCTCG 19
|||||
Db 425 ACATCGATCGCTCG 441

RESULT 4
BJ003054 630 bp mRNA linear EST 05-DEC-2001
LOCUS BJ003054 MF01SSA cDNA *Oryzias latipes* cDNA clone MF01SSA042E04 5',
DEFINITION mRNA sequence.
ACCESSION BJ003054
VERSION BJ003054.1 GI:17365174
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM *Oryzias latipes*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; *Oryzias*.
REFERENCE 1 (bases 1 to 630)
Kohara, Y., Shin-I, T., Kimura, T., Narita, T., Jinbo, T. and Takeda, H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
CONTACT: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genres.nig.ac.jp
LOCATION/Qualifiers

FEATURES

SOURCE

1. 630
/organism="Oryzias latipes"
/strain="Hd-rp"
/db_xref="taxon:8090"
/clone="MF01SA042E04"
/sex="mixture of female and male"
/issue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"

BASE COUNT 144 a 161 c 214 g 111 t

ORIGIN

Query Match 25.8%; Score 17; DB 10; Length 630;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ACATCTGATCGCTTCG 19
|||||

Db 575 AGATCTGATCGCTTCG 591

RESULT 5
LOCUS B022467 723 bp mRNA linear EST 05-DEC-2001
DEFINITION B022467 MF01SA cDNA Oryzias latipes cDNA clone MF01SA123D11 3',
mRNA sequence.
ACCESSION B022467
VERSION B022467.1 GI:17373869
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorphi; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
1 (bases 1 to 723)
Kohara,Y., Shin-I,T., Kimura,T., Narita,T., Jinbo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
Contact: Tadasi Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
location/Qualifiers
1. 723
/organism="Oryzias latipes"
/strain="Hd-rp"
/db_xref="taxon:8090"
/clone="MF01SA123D11"
/clone_lib="MF01SA cDNA"
/sex="mixture of female and male"
/issue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"

BASE COUNT 152 a 229 c 196 g 145 t 1 others

ORIGIN

Query Match 25.8%; Score 17; DB 10; Length 723;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ACATCTGATCGCTTCG 19
|||||

Db 537 ACATCTGATCGCTTCG 521

RESULT 5
LOCUS A0870164/c 778 bp DNA linear GSS 03-NOV-1999
DEFINITION A0870164 CUCI Rice BAC library (EcoRI) Oryza sativa genomic
clone nhebd0036h20r, DNA sequence.

ACCESSION A0870164
VERSION A0870164.1 GI:6220615
KEYWORDS GSS.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Fukariyoka; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrharioideae; Oryzaceae; Oryza.
1 (bases 1 to 778)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
JOURNAL
CONTACT: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAACACGATGACCATG
Class: BAC ends
High quality sequence start: 29
High quality sequence end: 522.
Location/Qualifiers
1. 778
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nhebd0036h20r"
/clone_lib="CUCI Rice BAC library (EcoRI)"
/issue_type="leaf"
/lab_host="E. coli DH10"
/note="Vector: pMAC10digo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monoculted rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mb (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa.
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9%. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

BASE COUNT 265 a 130 c 138 g 243 t 2 others

ORIGIN

Query Match 25.8%; Score 17; DB 12; Length 778;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 GACAAACGCTAAATAA 35
|||||

Db 446 GACAAACGCTAAATAA 330

RESULT 7
LOCUS BF306166 927 bp mRNA linear EST 21-NOV-2000
DEFINITION BF306166 601893015F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138922 5',
mRNA sequence.
ACCESSION BF306166
VERSION BF306166.1 GI:11253251

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 927)
TITLE NIH-MGC http://mgi.mcg.mcg.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rstrausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINC)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINC at: image.lnl.gov
Plate: LINC1048 row: m column: 04.

FEATURES
Location/Qualifiers
1..927
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:418922"
/clone_lib="NIH MGC 17"
/issue_type="rhabdomyosarcoma"
/lab_host="D1010H (phage-resistant)"
/note="Organ: muscle; Vector: pMT7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGTACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT
239 a 221 c 271 g 195 t 1 others

ORIGIN

Query Match 25.8%; Score 17; DB 10; Length 927;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cy 23 AAGGGTAAAAAGGG 49
db 813 AAGGGTAAAAAGGG 829

RESULT R
HE213126 211 bp mRNA linear EST 30-JUN-2000
LOCUS Iphr001569 brain cDNA library Icterus punctatus cDNA 5', mRNA
DEFINITION
ACCESSION HE213126
VERSION HE213126.1 GI:8844872
KEYWORDS
SOURCE EST.
ORGANISM channel catfish.
Icterus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
1 (bases 1 to 211)
Jin, Z., Karsli, A., Kocabas, A., Patterson, A., Li, P., Cao, D., Dunham, R.
and Liu, Z.
Transcriptome analysis of channel catfish: I. genes and expression
profiles from the brain
Unpublished (2000)
Contact: Liu, Z.J.
Fish Molecular Genetics and Biotechnology
Auburn University
203 Swingle Hall, Department of Fisheries, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.

FEATURES
Source Location/Qualifiers
1..211
/organism="Icterus punctatus"
/db_xref="taxon:7998"
/clone_lib="Brain cDNA library"
/note="Organ: Brain; Vector: pSport1; Site_1: Not1;
Site_2: SalI"

BASE COUNT
53 a 33 c 49 g 76 t

ORIGIN

Query Match 24.2%; Score 16; DB 9; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cy 20 ACACAAACGTAAAAA 35
db 192 ACACAAACGTAAAAA 207

RESULT 9
TA104E020/c 305 bp DNA linear GSS 13-DEC-2000
LOCUS T104E020
DEFINITION T1. brucei sheared genomic DNA clone 104402, reverse sequence,
genomic survey sequence.
ACCESSION AL462316 GI:11831561
VERSION AL462316
KEYWORDS
SOURCE GSS.
ORGANISM Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 305)
Hall, N., Bowman, S., Leonard, N.J., Boagett, J., Atkin, R.,
Chilindworth, C., Ormond, D., Harris, R., El Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE9927/4 CUTat 10.1) was mechanically sheared
to give a light size distribution (4 kb). The v.1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects). In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and R.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at <http://www.sanger.ac.uk/projects/T-brucei/>.

FEATURES
Source Location/Qualifiers
1..305
/organism="Trypanosoma brucei"
/strain="TRE927"
/db_xref="taxon:5691"
/clone="104402"

BASE COUNT
75 a 69 c 54 g 107 t

ORIGIN

Query Match 24.2%; Score 16; DB 12; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

cy 20 ACACAAACGTAAAAA 45
db 116 ACACAAACGTAAAAA 101

RESULT 10
TA104E020/c 427 bp DNA linear GSS 13-DEC-2000
LOCUS T104E020


```

/organism "Arabidopsis thaliana"
/db_xref "taxon:3702"
/clone "SALK_004649"
/feature "1b" "Arabidopsis thaliana TUNA insertion lines"
/note "PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TUNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tuna-protocols.html"
BASE COUNT      122 a      112 c      79 g      127 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 20 ACAAACGCTAATAAAA 35
|||||
1b 247 ACAAACGCTAATAAAA 222

RESULT 14
AM462196 441 bp mRNA linear EST 24-FEB-2000
LOCUS BP240008B10G12 Scores normalized bovine placenta Hos Taurus cDNA
DEFINITION
ACCESSION AM462196
VERSION AM462196.1 GI:7032464
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos Taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 441)
AUTHORS Lawin, H.A., Soares, M.B., Rebetz, M., Pardiñas, J., Liu, L. and Larson, J.H.
JOURNAL Unpublished (2000)
CONTACT: Lawin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
140 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 243 5998
Fax: 217 243 5617
Email: h.lawin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative: Animal Genome Resource Grant AG 99-2205-8534
to H. A. Lawin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trim: 9;
Cross-match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
PCR primers
FORWARD: TAATACGACGATCATAGG
REVERSE: ATTACGCTCATTAAG
Insert Length: 441 Std Error: 0.00
Plate: BP240008B10 row: G column: 12
Seq primer: AGCGATACCAATTCACACAGA
High quality sequence stop: 441.
location/Qualifiers
1..441
/organism="Bos Taurus"
/db_xref="taxon:9913"
/clone="BP240008B10G12"
/feature="1b" "Scores normalized bovine placenta"
/sex="female"
/lab_host="DHI03"
/note "Organism: Placenta; Vector: pTZ19ac; Site: 1; EcoRI;
Site 2: NotI; The cDNA library was contributed by the
Source Laboratory and it was constructed and normalized

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as described by Henaldi, M.F., Lemon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806.
BASE COUNT      141 a      77 c      94 g      139 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 50 TCTTCAATTCAGCT 65
|||||
1b 39 TCTTCAATTCAGCT 24

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RESULT 14
AM225607 442 bp mRNA linear EST 05-SEP-2000
LOCUS T2100586 KV0 Medicago truncatula cDNA clone pKV0-214, mRNA
DEFINITION
ACCESSION AM225607
VERSION AM225607.1 GI:6554903
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
Rosidae; eustosida; Fabales; Fabaceae; Papilionoideae; Titilaceae;
Medicago.
REFERENCE 1 (bases 1 to 442)
AUTHORS Vandenbosch, K., Inf, J., Beremand, P., Peng, H. and Ellis, L.
JOURNAL ESTs from uninculcated roots of Medicago truncatula
Unpublished (1999)
CONTACT: Vandenbosch, K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: Kate@mail.bio.tamu.edu
Other name: 38-KV0-214; date: 12/1/99; submitted to the database of
Expressed Sequence Tags (dbEST) on 12/10/99; More information is
available at http://chrysic.tamu.edu/medicago/.
Seq primer: SKMD (CTA gAA CTA gTA gAT CC).
location/Qualifiers
1..442
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV0-214"
/feature="1b" "KV0"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E. coli strain XL04R"
/note "Vector: pBluescript SK-; Site: 1; EcoRI; Site 2:
XhoI; cDNA was prepared from poly(A) enriched RNA. The cDNA
was directionally ligated into the unique Xk vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda Zap phage using Ex-assist
helper phage and propagated in XL04R cells."

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```

FEATURES
Source
1..442
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV0-214"
/feature="1b" "KV0"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E. coli strain XL04R"
/note "Vector: pBluescript SK-; Site: 1; EcoRI; Site 2:
XhoI; cDNA was prepared from poly(A) enriched RNA. The cDNA
was directionally ligated into the unique Xk vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda Zap phage using Ex-assist
helper phage and propagated in XL04R cells."
BASE COUNT      134 a      124 c      50 g      135 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 GAGATTCGATCCGTT 17
|||||
1b 395 GAGATTCGATCCGTT 380

```

RESULT 15
 A0500181 466 bp DNA linear GSS 29-APR-1999
 LOCUS VI578 min-3xHA/lacZ Insertion Library Saccharomyces cerevisiae
 DEFINITION genomic 5', DNA sequence.
 ACCESSION A0500181
 VERSION A0500181.1 GI:4705003
 KEYWORDS GSS.
 SOURCE Baker's yeast.
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 REFERENCE 1 (bases 1 to 466)
 Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,
 Deshaies, S.A., Cheung, K.-H., Sheehan, A., Symonakis, D., Jansen, R.,
 Umansky, L., Heidman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R.,
 Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
 Large-scale Analysis of the Yeast Genome by Transposon Tagging and
 Gene Disruption
 Unpublished (1999)
 JOURNAL Contact: Kumar A
 COMMENT Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
 Yale University
 P.O. Box 208103, New Haven, CT 06520-8103, USA
 Tel: 203 432 9949
 Fax: 203 432 6161
 Email: anuj.kumar@yale.edu
 Text of min-3xHA/lacZ insertion.
 Seq primer: GGCCTCTTCTTGCAGATAC
 Class: transposon-tagged.
 Location/Qualifiers
 1..466
 /organism="Saccharomyces cerevisiae"
 /db_xref="taxon:4932"
 /clone_lib="min-3xHA/lacZ Insertion Library"
 /lab_host="E. coli"
 /note="Vector: pHS6-Sal; A yeast genomic DNA library
 (lacking mitochondrial DNA) was prepared in pHS6-Sal;
 genomic DNA was size-fractionated (DNA of roughly 2-3 kb
 in length) prior to cloning. This library was
 subsequently mutagenized with a min-3xHA/lacZ
 multitransposon containing lacZ, URA3, and tetr resistance."
 BASE COUNT 177 a 118 c 69 g 101 t 1 others
 ORIGIN

Query Match 24.2%; Score 16; DB 12; Length 466;
 Best Local Similarity 100.0%; Pred. No. 1.4e-02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 20 ACMAACGGTAAAAA 35
 Db 280 ACMAACGGTAAAAA 295

RESULT 16
 AA696283 478 bp mRNA linear EST 23-APR-2001
 LOCUS GM05449.5prime GM Drosophila melanogaster ovary Bluescript
 DEFINITION Drosophila melanogaster cDNA clone GM05449 5prime, mRNA sequence.
 ACCESSION AA696283
 VERSION AA696283.1 GI:2698903
 KEYWORDS EST.
 SOURCE Fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 478)
 Harvey, D., Brokstedt, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G.M.
 BDGP/HMT Drosophila EST Project
 Unpublished (2001)
 COMMENT Contact: Stapleton, M.

BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: 54 row: F column: 1
 High quality sequence stop: 477.
 Location/Qualifiers
 1..478
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="GM05449"
 /clone_1ID="GM Drosophila melanogaster ovary Bluescript"
 /seq_stage="newly enclosed females: germlarium-stage 6"
 /lab_host="SOLR"
 /note="Organ: ovary; Vector: Bluescript SK; Site: 1; EcoRI;
 Site 2: XhoI; Constructed using Stratagene ZAP-cDNA
 Synthesis kit. Oligo dT-primed and directionally cloned at
 EcoRI and XhoI in Bluescript SK(+/-)."
 BASE COUNT 146 a 122 c 101 g 119 t
 ORIGIN

Query Match 24.2%; Score 16; DB 9; Length 478;
 Best Local Similarity 100.0%; Pred. No. 1.4e-02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 19 GACAAACGGTAAAAA 34
 Db 297 GACAAACGGTAAAAA 312

RESULT 17
 BG520697 479 bp mRNA linear EST 10-MAY-2001
 LOCUS ps50c03.y1 Trichinella spiralis ML CWSport JASMER Trichinella
 DEFINITION spiralis cDNA 5', mRNA sequence.
 ACCESSION BG520697
 VERSION BG520697.1 GI:13536124
 KEYWORDS EST.
 SOURCE Trichinella spiralis.
 ORGANISM Trichinella spiralis.
 Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
 Trichinellidae; Trichinella.
 REFERENCE 1 (bases 1 to 479)
 McCarter, J., Clifton, S., Chapell, B., Page, D., Martin, J., Wylie, T.,
 Dancie, M., Marra, M., Hillier, L., Kuehba, T., Theisand, B., Bowers, Y.,
 Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, H., R.,
 Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,
 M., Allen, K., Person, B., Swaller, J., Harvey, N., Schurk, R., Kohn, S.,
 Salm, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
 Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 COMMENT Contact: McCarter, JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 The library was constructed by Dr. Doug Jansner
 (djanse@vetmed.wsu.edu) at Washington State University, Dept. of
 Veterinary Microbiology and Pathology DNA Sequencing by: Washington
 University Genome Sequencing Center St. Louis.
 Seq primer: Sp6.
 Location/Qualifiers
 1..479
 /organism="Trichinella spiralis"
 /db_xref="taxon:6334"
 /clone_lib="Trichinella spiralis ML CWSport JASMER"
 /seq_stage="muscle stage larvae"
 /lab_host="DH10B"

/note="Vector: pCMVSPORT-7.000; Site_1: NotI; Site_2: SalI
: The library was constructed using mRNA isolated from
total RNA with oligo-dT cellulose. Total RNA was generated
from muscle larvae that were isolated from infected rats.
Larvae were liberated by pepsin/HCl digestion, incubated
with 1% SDS, treated with RNase and DNase to eliminate
host nucleic acid contamination, and purified on a Percoll
gradient. The T. spiralis isolate was obtained from
Dickson Despresmier (Columbia University). The library was
provided by Dr. David Janssen (djangm@wisc.edu) and
colleagues at Washington State University. DNA Sequencing
by: Washington State University Genome Sequencing Center
Lewis."

BASE COUNT 158 a 80 c 109 g 142 t
ORIGIN

Query Match 24.2%; Score 16; DH 10; Length 479;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 40 AAAAAAGGAGTAGATT 45
|||||

DB 400 AAAAAAGGAGTAGATT 415

RESULT 18

HE444884 479 bp mRNA linear EST 25-JUN-2000

LOCUS WHE1129_F06_K1125 wheat etiolated seedling root normalized cDNA

DEFINITION Library Triticum aestivum cDNA clone WHE1129_F06_K11, mRNA

ACCESSION HE444884

VERSION HE444884.1 GI:9444435

KEYWORDS EST

SOURCE broad wheat

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.

REFERENCE 1 (bases 1 to 479)
Anderson, O.D., Zhao, S., Chou, D.W., Close, T.J., Fenton, R.D., Han

P.S., Hsiao, C.C., Kang, Y., Izzo, G.R., Miller, R., Nguyen, H.T.,
Rauscher, C.J., Seaton, C.L., Tong, J.C., and Zhang, D.

The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library

Unpublished (2000)

JOURNAL Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773
Fax: 5105595418

Email: anderson@w.arsda.gov

Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20

Seq primer: Stradagene SK primer.

Location/Qualifiers

1..479
/organism="Triticum aestivum"

/db_xref="taxon:4565"

/clone="WHE1129_F06_K11"

/clone_lib="Wheat etiolated seedling root normalized cDNA
library"

/tissue_type="Root"

/dev_stage="Five day old etiolated seedling"

/lab_host="E. coli DH10H"

/note="Vector: lambda Uni-ZAP XR, excised phagemid
pluscript SK; Site_1: KORI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
tystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and

poly(A) RNA were prepared, a cDNA library was made in the
T3 Clontech lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pluscript phagemids before
normalization was carried out. The mass extinction of
phagemid library and normalization were done in RT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the (D)
Anderson lab (all other authors)."

BASE COUNT 119 a 114 c 126 g 120 t
ORIGIN

Query Match 24.2%; Score 16; DH 10; Length 479;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 7 CTGGATCGCTGGACA 22
|||||

DB 225 CTGGATCGCTGGACA 240

RESULT 19

HI582395

LOCUS HI582395 485 bp mRNA linear EST 06-SEP-2001

DEFINITION RH20445_Sprime RH Drosophila melanogaster normalized head p1c-1

Drosophila melanogaster cDNA clone RH20445.5 similar to Y115:
Pha00002913 Go: Integral plasma membrane protein (GO:0005887);
hydrogen/oxygen/oxide symporter (GO:0005427); hydrogen/oxygen/oxide
symporter (GO:0005427); transporter (GO:0005215); integral plasma
membrane protein (GO:0005887); by: mRNA sequence.

ACCESSION HI582395

VERSION HI582395.1 GI:15473817

KEYWORDS EST

SOURCE fruit fly

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 485)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson

J., Chang, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George

R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mista, S.,

Mungall, C.J., Nuno, J., Pacleb, J., Parnas, V., Park, S.,
Phonathanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin

G.M.
BACP/HHMT RH Drosophila EST Project

Unpublished (2001)

JOURNAL Contact: Stapleton, M.

BDGP Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: http://www.fruitfly.org/EST_est/fruitfly.berkeley.edu

Plate: RH:204 Row: D Column: 9

High quality sequence stop: 411.

Location/Qualifiers

1..485
/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="RH20445"

/clone_lib="RH Drosophila melanogaster normalized head
p1c-1"

/sex="male and female"

/dev_stage="Adult"

/lab_host="DH5-alpha Tona"

/note="Organ: head; Vector: p1c1; Site_1: XhoI; Site_2:
HinfI; Library was kindly generated by Piero Garattini at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

BASE COUNT 131 a 121 c 106 g 127 t
ORIGIN

Query Match 24.2% Score 16; DB 10; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GACCAAAACGCTAAAA 34
 |||||||
 DB 340 GACCAAAACGCTAAAA 355

RESULT 20
 LOCUS B98126 486 bp DNA linear GSS 31-MAR-1998
 DEFINITION F24A161F6 IGF Arabidopsis thaliana genomic clone F24A16, DNA
 sequence.
 ACCESSION B98126
 VERSION B98126.1 GI:3000205
 KEYWORDS GSS.
 SOURCE Thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 486)
 Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Linher, K., Golden, K.,
 Berry, K., Granger, D., Suh, E., Wible, C., Adams, M.D. and Venter
 , J.C.
 TITLE A PAC End Sequence Database for Identifying Minimal Overlaps in
 Arabidopsis Genomic Sequencing. Update 3
 JOURNAL Unpublished (1997)
 COMMENT Contact: Steve Rounsley
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: rounsley@tifgr.org
 Seq primer: M13-21
 Class: PAC ends
 High quality sequence stop: 486.
 Location/Qualifiers
 1..486
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="F24A16"
 /clone_lib="IGF"
 /sex="Dermaphrodite"
 /note="Vector: BelovPAC11; Site_1: EcoRI; Site_2: EcoRI;
 Produced by Thomas Altmann"
 BASE COUNT 149 a 88 c 90 g 159 t
 ORIGIN

Query Match 24.2% Score 16; DB 12; Length 486;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCACAAAACGCTAAAA 33
 |||||||
 DB 380 GCACAAAACGCTAAAA 395

RESULT 21
 LOCUS B1607662 516 bp mRNA linear EST 07-SEP-2001
 DEFINITION RH74766 Sp1me RH Drosophila melanogaster normalized head pf1c-1
 Drosophila melanogaster cDNA clone RH74766 5 similar to yin:
 Pham0002913 GO:0005427 integral plasma membrane protein (GO:0005887);
 hydrogen/oilpeptide symporter (GO:0005427); hydrogen/oilpeptide
 symporter (GO:0005427); transporter (GO:0005215); integral plasma
 membrane protein (GO:0005887); hy, mRNA sequence.
 ACCESSION B1607662
 VERSION B1607662.1 GI:15503187
 KEYWORDS EST.

SOURCE
 ORGANISM Fruit fly.
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 516)
 Rounsley, S.D., Brokstein, P., Hong, L., Tyler, D., Berman, R., Carlson
 , J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
 , R., Gonzalez, M., Guatin, H., Harris, N., Li, P., Liao, G., Mista, S.,
 Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
 Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin
 , G.M.
 TITLE RBCF/HMT RH Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: RH 747 row: F column: 6
 High quality sequence stop: 414.
 Location/Qualifiers
 1..516
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH74766"
 /clone_lib="RH Drosophila melanogaster normalized head
 pf1c-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DHS-alpha T0A"
 /note="Organ: head; Vector: pF1c1; Site_1: XhoI; Site_2:
 BamHI. Library was kindly generated by Peter Garinetti at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."
 BASE COUNT 142 a 130 c 112 g 132 t
 ORIGIN

Query Match 24.2% Score 16; DB 10; Length 516;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GACCAAAACGCTAAAA 34
 |||||||
 DB 340 GACCAAAACGCTAAAA 355

RESULT 22
 LOCUS B1584222 532 bp mRNA linear EST 06-SEP-2001
 DEFINITION RH23234 Sp1me RH Drosophila melanogaster normalized head pf1c-1
 Drosophila melanogaster cDNA clone RH23234 5 similar to yin:
 Pham0002913 GO:0005427 integral plasma membrane protein (GO:0005887);
 hydrogen/oilpeptide symporter (GO:0005427); hydrogen/oilpeptide
 symporter (GO:0005427); transporter (GO:0005215); integral plasma
 membrane protein (GO:0005887); hy, mRNA sequence.
 ACCESSION B1584222
 VERSION B1584222.1 GI:15475644
 KEYWORDS EST.
 SOURCE Fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 532)
 Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, R., Carlson
 , J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
 , R., Gonzalez, M., Guatin, H., Harris, N., Li, P., Liao, G., Mista, S.,
 Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
 Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin
 , G.M.
 TITLE RBCF/HMT RH Drosophila EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: RH 747 row: F column: 6
 High quality sequence stop: 414.
 Location/Qualifiers
 1..516
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH74766"
 /clone_lib="RH Drosophila melanogaster normalized head
 pf1c-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DHS-alpha T0A"
 /note="Organ: head; Vector: pF1c1; Site_1: XhoI; Site_2:
 BamHI. Library was kindly generated by Peter Garinetti at
 the RIKEN. The library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."
 BASE COUNT 142 a 130 c 112 g 132 t
 ORIGIN

JOURNAL, Unpublished (2001)
Contact: Stapleton, M

ACCESSION H1612678
 VERSION H1612678.1 GI:15508210
 KEYWORDS EST.
 SOURCE Fruit fly.
 ORGANISM *Drosophila melanogaster*
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; *Drosophila*.
 REFERENCE 1 (bases 1 to 571)
 AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guatin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C. J., Nuno, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celinker, S. and Rubin, C. M.
 TITLE BDGP/HIMI RH *Drosophila* EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: RH 416 row: C column: 2
 High quality sequence stop: 505.
 Location/Qualifiers
 1..571
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH41626"
 /clone_lib="RH Drosophila melanogaster normalized head
 P1c-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DHS-alpha Tona"
 /note="Organ: head; Vector: pF1c; Site_1: XhoI; Site_2: BamHI. Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
 BASE COUNT 152 a 148 c 122 g 149 t
 ORIGIN
 Query Match 24.2% Score 16; DB 10; Length 571;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 UY 19 GACAAACGGTAAAAA 34
 ||||||||||||||||
 DB 330 GACAAACGGTAAAAA 345
 RESULT 26
 TA55H110/c
 LOCUS
 DEFINITION T. brucei sheared genomic DNA clone 55H11, reverse sequence.
 ACCESSION AL456183
 VERSION AL456183.1 GI:11857054
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE 1 (bases 1 to 574)
 AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doaggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M. A., Barrell, B. G.
 TITLE Direct Submission
 JOURNAL Submitted (10-JMC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhs@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TRE927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J. C. (Making small insert libraries for a whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nhs@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available at <http://www.sanger.ac.uk/Projects/T-brucei/>.
 Location/Qualifiers
 1..574
 /organism="Trypanosoma brucei"
 /strain="TRE927"
 /db_xref="taxon:5691"
 /clone="55H11"
 /clone_lib="RH Drosophila melanogaster normalized head
 P1c-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DHS-alpha Tona"
 BASE COUNT 184 a 113 c 116 g 161 t
 ORIGIN
 Query Match 24.2% Score 16; DB 12; Length 574;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 UY 20 ACMAAACGGTAAAAA 35
 ||||||||||||||||
 DB 193 ACMAAACGGTAAAAA 178
 RESULT 27
 B1565318
 LOCUS
 DEFINITION B1565318 580 bp mRNA linear EST 06-SEP-2001
 RH53067.5prline RH *Drosophila* melanogaster normalized head P1c-1
Drosophila melanogaster cDNA clone RH53067 5 similar to yin:
 P8a0002913 GO: [integral plasma membrane protein (GO:0005887);
 hydrogen/oilseed/plasma symporter (GO:0005427); hydrogen/oilseed/plasma
 symporter (GO:0005427); transporter (GO:0005215); integral plasma
 membrane protein (GO:0005887), mRNA sequence.
 B1565318
 ACCESSION B1565318
 VERSION B1565318.1 GI:15454510
 KEYWORDS EST.
 SOURCE Fruit fly.
 ORGANISM *Drosophila melanogaster*
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; *Drosophila*.
 REFERENCE 1 (bases 1 to 580)
 AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guatin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C. J., Nuno, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celinker, S. and Rubin, C. M.
 TITLE BDGP/HIMI RH *Drosophila* EST Project
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Plate: RH 630 row: F column: 7
 High quality sequence stop: 515.
 Location/Qualifiers
 1..580
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH63067"
 /clone_lib="RH Drosophila melanogaster normalized head
 P1c-1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DHS-alpha Tona"

/note="Organ: head; Vector: pPIC1; Site_1: XhoI; Site_2: BamHI. Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cte recombinase. Plasmid cDNA library."

BASE COUNT 155 a 151 c 124 g 150 t

ORIGIN

Query Match 24.2% Score 16; DB 10; Length 580;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 19 GACAAACCGTAAAAA 34
 |||

DB 340 GACAAACCGTAAAAA 355

RESULT 28
LOCUS A1485800
DEFINITION EST244121 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
ACCESSION A1485800
VERSION A1485800.1 GI:381171
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
 Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum;
 Lycopersicon.
REFERENCE 1 (bases 1 to 590)
 Alcala, J., Vrebalov, J., White, R., Matern, A., Viston, T., Holt, L. E.,
 Liang, F., Upton, J., Komig, C. M., Craven, M. B., Fujii, C. Y., Bowman
 C. L., Nicotian, W., Fraser, C. M., Venter, J. C., Martin, G. R., Tanksley
 S. D. and Giovannoni, J.
 Generation of ESTs from tomato carpel tissue
 Unpublished (1999)
TITLE Contact: TUGI
JOURNAL Clemson University Genomics Institute
COMMENT Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>.
FEATURES
SOURCE 1..590
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLE04117"
 /clone_1lb="tomato ovary, TAMU"
 /tissue_type="carpel"
 /dev_stage="5 days post-anthesis to 5 days post-anthesis"
 /lab_host="XLI-Blue MRF"
 /note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
 XhoI; cldo - tomato Carpel EST library. OligodT-primed and
 directionally cloned cDNA in vector lambda ZAP II with 5'
 and 3' ends located at the EcoRI and XhoI sites,
 respectively."

BASE COUNT 175 a 92 c 115 g 208 t

ORIGIN

Query Match 24.2% Score 16; DB 9; Length 590;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 47 CCGCTACGCAATCA 62
 |||

DB 552 CCGCTACGCAATCA 567

RESULT 29
LOCUS B1630819
DEFINITION RH60131. Sprime RH Drosophila melanogaster normalized Head pPIC1

Drosophila melanogaster cDNA clone RH60131 5 similar to yin:
 Phen0002913 GO:lipid integral plasma membrane protein (GO:0005887);
 hydrogen/oilpeptide symporter (GO:0005427); hydrogen/oilpeptide
 symporter (GO:0005427); transporter (GO:0005215); integral plasma
 membrane protein (GO:0005887); mRNA sequence.

ACCESSION B1630819
VERSION B1630819.1 GI:15531029
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 600)
 Stapleton, M., Broks, P., Hong, L., Tyler, D., Herman, B., Carlson
 J., Champ, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George
 R., Gonzalez, M., Guerin, H., Harris, N., Li, P., Lao, G., Misra, S.,
 Mungall, C. J., Nunoo, J., Parle, D., Paras, V., Park, S.,
 Pham, N., S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and Rubin
 G. M.
 BDBP/EMBL RH Drosophila EST Project
 Unpublished (2001)
TITLE Contact: Stapleton, M.
JOURNAL BDBP
COMMENT Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.italy.berkeley.edu>
 Plate: RH 601 row: C column: 7
 High quality sequence stop: 532.
FEATURES
SOURCE 1..600
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="RH60131"
 /clone_1lb="RH Drosophila melanogaster normalized head
 pPIC1"
 /sex="male and female"
 /dev_stage="Adult"
 /lab_host="DH5-alpha Tona"
 /note="Organ: head; Vector: pPIC1; Site_1: XhoI; Site_2:
 BamHI. Library was kindly generated by Piero Carninci at
 the RIKEN. The library was normalized and excised using
 Cte recombinase. Plasmid cDNA library."
BASE COUNT 157 a 136 c 130 g 155 t
ORIGIN 2 others

Query Match 24.2% Score 16; DB 10; Length 600;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 19 GACAAACCGTAAAAA 34
 |||

DB 340 GACAAACCGTAAAAA 355

RESULT 30
LOCUS B1568118
DEFINITION RH39495. Sprime RH Drosophila melanogaster normalized head pPIC1

B1568118 611 bp mRNA linear EST 06-SEP-2001
 RH39495. Sprime RH Drosophila melanogaster normalized head pPIC1
 Drosophila melanogaster cDNA clone RH39495 5 similar to yin:
 Phen0002913 GO:lipid integral plasma membrane protein (GO:0005887);
 hydrogen/oilpeptide symporter (GO:0005427); hydrogen/oilpeptide
 symporter (GO:0005427); transporter (GO:0005215); integral plasma
 membrane protein (GO:0005887); mRNA sequence.

ACCESSION B1568118
VERSION B1568118.1 GI:15457310
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.


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|||||
Db      340 GACAAACGGTAAAAA 355

RESULT 35
LOCUS   AA202447
DEFINITION LD02644.5prime LD Drosophila melanogaster embryo Bluescript.
ACCESSION AA202447
VERSION   AA202447
KEYWORDS  EST.
SOURCE    fruit fly.
ORGANISM  Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
           Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
           Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 649)
AUTHORS   Harvey,D., Brookslein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
           Lewis,S., and Rubin,G.M.
TITLE      BDGF/HMT Drosophila EST Project
JOURNAL    Unpublished (2001)
COMMENT    Contact: Stapleton, M.
           BDCP
           Lawrence Berkeley National Lab
           One Cyclotron Rd, Berkeley, CA 94720, USA
           Fax: 510 486 6798
           Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
           Plate: 26 row: D column: 8
           High quality sequence stop: 601.
FEATURES
  source
    1..649
    /organism="Drosophila melanogaster"
    /db_xref="MIM:EST:5021002311"
    /db_xref="taxon:7227"
    /clone_lib="LD Drosophila melanogaster embryo Bluescript"
    /sex="male and female"
    /dev_stage="0 to 24 hours mixed stage embryonic"
    /note="organ: embryo; Vector: Bluescript SK; Site_1: EORI;
    Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
    Synthesis kit. Oligo dt-primed and directionally cloned at
    EcoRI and XhoI in Bluescript SK(+/-)"
BASE COUNT  169 a 163 c 145 g 172 t
ORIGIN
Query Match      24.2% Score 16; DB 9; Length 649;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 GACAAACGGTAAAAA 34
Db      415 GACAAACGGTAAAAA 330

RESULT 36
LOCUS   RI229347
DEFINITION RI229347 653 bp mRNA linear EST 11-JUL-2001
           RE27113.5prime RE Drosophila melanogaster normalized Embryo pf1c-1
           Drosophila melanogaster cDNA clone RE27113 5 similar to yin:
           FBa0002913 'transposon' located on: X 4A1-4A1:: 04/12/2001, mRNA
           sequence.
ACCESSION RI229347
VERSION   RI229347
KEYWORDS  EST.
SOURCE    fruit fly.
ORGANISM  Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
           Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
           Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 653)
AUTHORS   Stapleton,M., Brookslein,P., Hong,L., Tyler,D., Herman,B., Carlson

```

```

|||||
TITLE    BDGF/HMT RE Drosophila EST Project
JOURNAL    Unpublished (2001)
COMMENT    Contact: Stapleton, M.
           BDCP
           Lawrence Berkeley National Lab
           One Cyclotron Rd, Berkeley, CA 94720, USA
           Fax: 510 486 6798
           Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
           Plate: RE 271 row: B column: 1
           High quality sequence stop: 585.
FEATURES
  source
    1..653
    /organism="Drosophila melanogaster"
    /db_xref="taxon:7227"
    /clone_lib="RE Drosophila melanogaster normalized Embryo
    pf1c-1"
    /sex="male and female"
    /dev_stage="0-24 hours mixed stage embryonic"
    /note="organ: embryo; Vector: pf1c1; Site_1: XhoI; Site_2:
    BamHI; library was kindly generated by Pietro Garinucci at
    the RIKEN. The library was normalized and excised using
    Cre recombinase. Plasmid cDNA library."
BASE COUNT  173 a 165 c 144 g 171 t
ORIGIN
Query Match      24.2% Score 16; DB 10; Length 653;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 GACAAACGGTAAAAA 34
Db      339 GACAAACGGTAAAAA 354

RESULT 37
LOCUS   AW690071/c
DEFINITION NF028A06ST1F1000 Developing stem Medicago truncatula cDNA clone
ACCESSION AW690071
VERSION   AW690071
KEYWORDS  EST.
SOURCE    barrel medic.
ORGANISM  Medicago truncatula
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eurosids 1; Fabiales; Fabaceae; Papilionoideae; Fritilliae;
           Medicago.
REFERENCE 1 (bases 1 to 660)
AUTHORS   He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Beall,
           C.J., Flores,H.R., Iman,J.T., Weller,J.W., May,G.D. and Dixon,
           R.A.
TITLE      Expressed Sequence Tags from the Samuel Roberts Noble Foundation
           Medicago truncatula stem library
JOURNAL    Unpublished (2000)
COMMENT    Contact: Dixon RA
           Plant Biology Division
           The Samuel Roberts Noble Foundation
           2510 Sam Noble Parkway, Ardmore, OK 73402, USA
           Tel: 580 221 7302
           Fax: 580 221 7360
           Email: radixon@noble.org
           Insert length: 660 Std Error: 0.00
           Plate: 028 row: A column: 06
           Seq primer: TCACACAGGAACGCAATGAC.
           Location/Qualifiers

```


497-598)"
 /db_xref:"taxon:5855"
 /clone_id:"By MN #30"
 /dev_stage:"asexual blood forms"
 /lab_host:"Salimif bollywoodis"
 /note:"vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP, Site 1: EcoR V; Site 2: EcoR V; host leukocytes were extracted from P. vivax infected blood using the following methods: first, infected blood was activated by the addition of 0.5 ml of ACP (40mg/ml) per 10 ml blood. The blood was passed over a column of acid washed 0.1 mm glass beads, then through a plasmidipur filter, followed by passage through a column of pre-wet Whatman Cell powder (1:2 ratio volume of blood to Cell), and finally centrifuged through a 50% Percoll density cushion. Purified DNA was digested with many bean nuclease in the presence of 44% formamide at 50°C as described (Verrick, K.B., Imborski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). Digested DNA was blunt ended using T4 DNA polymerase and size fractionated over a Sepharose CL-2B column. Fractions in the size range 500bp-4kb were ligated into the Eco RV site of phagescript SK(+), and E. coli XL-10 Gold transformed with the ligation mixture."

BASE COUNT 247 a 116 c 161 g 154 t 1 others
 ORIGIN

Query Match 24.2% Score 16; DB 12; Length 679;
 Best Local Similarity 100.0%; Prod. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACMAAACGCTAATAA 35
 ||||||||||||||||
 Db 217 ACMAAACGCTAATAA 212

RESULT 43
 LACUS
 DEFINITION
 H1582214 681 bp mRNA linear EST 06-SEP-2001
 RH20171.5ptine RH Drosophila melanogaster normalized Head p1c-1
 Drosophila melanogaster cDNA clone RH20171 5 similar to yin:
 FBA0002913 GO: integral plasma membrane protein (GO:0005887);
 hydrogon/coligopeptide symporter (GO:0005427); hydrogon/coligopeptide
 symporter (GO:0005427); transporter (GO:0005215); integral plasma
 membrane protein (GO:0005887); hy, mRNA sequence.
 H1582214
 H1582214.1 GI:15471636
 EST
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 681)
 Stapleton, M., Brooks, P., Hong, L., Tyler, D., Berman, B., Carlson,
 J., Champ, M., Chavez, C., Dorsett, Y., Farfan, D., Fiske, E., George,
 R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S.,
 Monaldi, C., Nuno, J., Pachab, J., Paragas, V., Park, S.,
 Phonsavong, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and Rubin,
 C.M.
 RDPG/HMT RH Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 MDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Phone: RH 201 row: F column: 11
 high quality sequence stop: 510
 Location/Qualifiers
 1. 681
 /organism:"Drosophila melanogaster"

/db_xref:"taxon:7227"
 /clone_id:"RH20171"
 /clone_id:"RH Drosophila melanogaster normalized Head
 p1c-1"
 /sex:"male and female"
 /dev_stage:"Adult"
 /lab_host:"Drosophila Tona"
 /note:"Organ: head; Vector: p1c-1; Site 1: XhoI; Site 2:
 BamHI; Library was kindly generated by Piero Garini at
 the RIKEN the library was normalized and excised using
 Cre recombinase. Plasmid cDNA library."

BASE COUNT 175 a 171 c 152 g 183 t
 ORIGIN

Query Match 24.2% Score 16; DB 10; Length 681;
 Best Local Similarity 100.0%; Prod. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCAAAACGCTAATAA 34
 ||||||||||||||||
 Db 340 GCAAAACGCTAATAA 355

RESULT 44
 LACUS
 DEFINITION
 BH432863 690 bp mRNA linear EST 25-OCT-2001
 BH432863 RIKEN full-length cDNA clone, adult male hippocampus Mus
 musculus cDNA clone C630048020 3', mRNA sequence.
 BH432863
 BH432863.2 GI:16424253
 EST
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse:
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 690)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Harai, A.,
 Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,
 M., Koyama, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
 Okazaki, Y., Okita, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,
 D., Shibata, K., Shinagawa, A., Shiraki, T., Souabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toy, T.,
 Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 On Jul 18, 2000 this sequence version replaced 91:9272590.
 Contact: Yoshinori Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 240-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res-qsc@riken.go.jp,
 URL: http://genome-qsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayashizaki, M., Sugahara, Y., Shibata, K., Itoh,
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system: 484-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakaki, I., Aizawa

Eudaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliceae

Medicago.

1 (bases 1 to 587)

[illegible]

LOCUS	BF642214	680 bp	RNA	linear	EST 19-DEC-2000
DEFINITION	NE067C04.INF103	Insect herbivory	Medicago truncatula	cDNA clone	
ACCESSION	NE067C04IN 5	RNA sequence.			
VERSION	BF642214				
KEYWORDS	BF642214.1	GI:11906372			
SOURCE	EST.				
ORGANISM	barrel medic.				
REFERENCE	Medicago truncatula				
AUTHORS	Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eustosids I: Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.				
TITLE	1 (bases 1 to 680)				
JOURNAL	Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.				
COMMENT	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library unpublished (2000)				
FEATURES	Contact: Korth K				
SOURCE	Dept. of Plant Pathology				
	University of Arkansas				
	217 Plant Science Building, Fayetteville, AR 72701, USA				
	Tel: 501 575 5191				
	Fax: 501 575 7601				
	Email: korthcomp.uark.edu				
	Insert Length: 680	Std Error: 0.00			
	Plate: 067	row: C column: 04			
	Seq primer: TCACACGGAACACGCTATGAC.				
	Location/Qualifiers				
	1..680				
	/organism="Medicago truncatula"				
	/db_xref="taxon:3880"				
	/clone_lib="NF067C04IN"				
	/tissue_type="local and systemic leaves"				
	/dev_stage="mature"				
	/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."				
BASE COUNT	182 a	139 c	174 g	180 t	5 others
ORIGIN					
Query Match	38.5%	Score 25.4:	DB 10:	Length 680:	
Best Local Similarity	68.6%	Pred. No. 1e+02:			
Matches	35: Conservative	0: Mismatches	16: Indels	0: Gaps	0:
Oy	4	GATTCGATCCGTTGCAGCAACGATAAAGCGTACATTACCGTCTCA	54		
Db	70	TTT TTTTTTTTTTTT TTT TTT TTT TTT TTT TTT TTT	120		
RESULT 12					
LOCUS	AM689706	688 bp	RNA	linear	EST 15-JUN-2000
DEFINITION	NE023D11ST.1F1000	Developing stem	Medicago truncatula	cDNA clone	
ACCESSION	NE023D11ST 5'	RNA sequence.			
VERSION	AM689706				
KEYWORDS	AM689706.1	GI:7564442			
SOURCE	EST.				
ORGANISM	barrel medic.				
REFERENCE	Medicago truncatula				
AUTHORS	Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eustosids I: Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.				
	1 (bases 1 to 680)				
	He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.				
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library				

JOURNAL
COMMENT

(unpublished (2000)
Contact: Dixon KA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radikom@noble.org
Insert length: 688 Std Error: 0.00
plate: 023 row: D column: 1)
Seq primer: TCACACAGGAAACGATATGAC.

FEATURES

Location/Qualifiers
1..688

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF023011ST"

/clone_lib="Developing stem"

/tissue_type="stem"

/dev_stage="pooled developmental"

/note="Vector: Lambda Zap; Contains a mixture of
intermodal stem segments"

BASE COUNT 181 a 139 c 176 g 189 t 3 others

ORIGIN

Query Match 48.5%; Score 25.4; DB 9; Length 688;
Best Local Similarity 68.6%; Pred. No. 1e+02;
Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

4 GATCTGATCGCTTCGACAAACGGTAAAGCGGTACATTACGCTCTA 54

111 1 11111111 11111 11111 11111111

57 GATCTGATCGCTTCGACAAACGGTAAAGCGGTACATTACGCTCTA 107

RESULT 13

LOCUS M6645754

DEFINITION EST007473 KX3 Medicago truncatula cDNA clone pKV3 47B11 5' end,

ACCESSION M6645754

VERSION M6645754.1 GI:13780866

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustroids 1; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.

1 (bases 1 to 777)

REFERENCE Vandenbosch, K., Endre, G., Hu, J., Beremand, P., Town, C.D., Bowman
C.L., Graven, M.H., Cho, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula 72 h after Rhizobium
inoculation, 2001

1 (unpublished (2001)

CONTACT: Vandenbosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: katowall@bio.tamu.edu

M39416c 1168 sequence name: MTRC0606TK More information is
available at: www.medicago.org

Seq primer: Skm04 (CTA GAA CTA Gtg GAT CC).

Location/Qualifiers

1..777

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="pKV3 47B11"

/clone_lib="KV3"

/tissue_type="Seedling roots"

/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"

FEATURES

SOURCE

1..777

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="pKV3 47B11"

/clone_lib="KV3"

/tissue_type="Seedling roots"

/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"

/lab_host="E. coli strain XL100"

/note="Vector: pBluescript SK+; Site 1: EORI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the unique XhoI vector from
Stratagene and packaged using giga-pack III gold packaging
extracts. plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL100 cells."

BASE COUNT 206 a 158 c 196 g 217 t

ORIGIN

Query Match 38.5%; Score 25.4; DB 10; Length 777;
Best Local Similarity 68.6%; Pred. No. 1e+02;
Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

4 GATCTGATCGCTTCGACAAACGGTAAAGCGGTACATTACGCTCTA 54

111 1 11111111 11111 11111 11111111

51 GATCTGATCGCTTCGACAAACGGTAAAGCGGTACATTACGCTCTA 101

RESULT 14

LOCUS A1260450

DEFINITION A1260450 459 bp mRNA linear EST 19-APR-2001

lP04321.5prime LP Drosophila melanogaster larval-early pupal pOT2

Drosophila melanogaster cDNA clone lP04321 5prime similar to
M59076; Maf49 Fhq0010241 P1D9457871 SWISS-PROT:Q00449, mRNA
sequence.

ACCESSION A1260450

VERSION A1260450.1 GI:3867975

KEYWORDS EST.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 459)

REFERENCE Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HMI Drosophila EST project
Unpublished (2001)

CONTACT: Stapleton, M.

BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estfruitfly.berkeley.edu
Plate: 43 row: B column: 9
High quality sequence stop: 422.

Location/Qualifiers

1..459

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="lP04321"

/clone_lib="LP Drosophila melanogaster larval-early pupal
pOT2"

/sex="male and female"

/dev_stage="larvae-pupae"

/lab_host="DH5-alpha"

/note="Organ: whole body; Vector: pOT2; Site 1: EORI;
Site 2: XhoI. Sized fractionated cDNAs were directly
ligated into pOT2. Plasmid cDNA library."

BASE COUNT 97 a 127 c 147 g 88 t

ORIGIN

Query Match 48.2%; Score 25.2; DB 9; Length 459;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 36; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

8 TGGATCGTTCGACAAACGGTAAAGCGGTACATTACGCTCTA 61

1111111 11111 11111 11111 11111 11111

66 TGGATCGTTCGACAAACGGTAAAGCGGTACATTACGCTCTA 119

RESULT 15

AA698485

LOCUS

DEFINITION

AA698485 521 bp mRNA linear EST 19-Apr-2001
 HL04775: 5prime HL Drosophila melanogaster head Bluescript
 Drosophila melanogaster cDNA clone HL04775 5prime similar to
 M59076: Mdt49 Ebn0010241 Ptd:q157871 SWISS-PROT:Q00449, mRNA
 sequence.

ACCESSION

AA698485

VERSION

AA698485.1 GI:2701414

KEYWORDS

EST

SOURCE

fruit fly

ORGANISM

Drosophila melanogaster

REFERENCE

Eukaryota; Metazoa; Arthropoda; Insecta; Diptera; Brachycera;

AUTHORS

Petrykova; Neopterygota; Endopterygota; Diptera; Brachycera;

TITLE

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

JOURNAL

1 (bases 1 to 521)

COMMENT

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G.M.
 BGGP/HMT Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 BGGP

FEATURES

source

FEATURES

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 Plate: 47 row: 6 column: 3
 High quality sequence stop: 378.
 Location/Qualifiers

FEATURES

1..521

FEATURES

/organism="Drosophila melanogaster"

FEATURES

/db_xref="taxon:7227"

FEATURES

/clone="HL04775"

FEATURES

/sex="male and female"

FEATURES

/dev_stage="adult"

FEATURES

/lab_host="SOLR"

FEATURES

/note="Organ: head-brain & sensory organ; Vector:
 Bluescript SK; Site_1: EcoRI; Site_2: XhoI; Constructed
 using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-pripped
 and directionally cloned at EcoRI and XhoI in Bluescript
 SK(+/-)"

FEATURES

BASE COUNT 111 a 134 c 153 g 123 t

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Search completed: November 5, 2002, 08:09:53
 Job time : 808.027 secs

Query Match 100.0%; Score 66; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 6.5e-14;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGATCGATCGCTTGGACAAACGGTAAAGCGGTACGATTCGCTAGCAATT 60
 |||
 DB 1 TCAGATCGATCGCTTGGACAAACGGTAAAGCGGTACGATTCGCTAGCAATT 60

QY 61 CAGCTG 66
 |||
 DB 61 CAGCTG 66

RESULT 2
 AX204116 66 bp DNA linear PAT 30-AUG-2001
 LOCUS AX204116
 DEFINITION Sequence 24 from Patent WO0153502.
 ACCESSION AX204116
 VERSION AX204116.1 GI:15392477
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 AUTHORS Bruce, W.B. and Niu, X.
 TITLE Novel root-preferred promoter elements and methods of use
 JOURNAL Patient: WO 0153502-A 24-JUL-2001;
 PIONEER HI-BRED INTERNATIONAL, INC. (US)
 FEATURES
 source
 1..66
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 21 a 14 c 16 g 15 t
 ORIGIN

Query Match 100.0%; Score 66; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 6.5e-14;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGATCGATCGCTTGGACAAACGGTAAAGCGGTACGATTCGCTAGCAATT 60
 |||
 DB 1 TCAGATCGATCGCTTGGACAAACGGTAAAGCGGTACGATTCGCTAGCAATT 60

QY 61 CAGCTG 66
 |||
 DB 61 CAGCTG 66

RESULT 3
 AX204095 66 bp DNA linear PAT 30-AUG-2001
 LOCUS AX204095
 DEFINITION Sequence 4 from Patent WO0153502.
 ACCESSION AX204095
 VERSION AX204095.1 GI:15392454
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 AUTHORS Bruce, W.B. and Niu, X.
 TITLE Novel root-preferred promoter elements and methods of use
 JOURNAL Patient: WO 0153502-A 26-JUL-2001;
 PIONEER HI-BRED INTERNATIONAL, INC. (US)
 FEATURES
 source
 1..66
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="random oligonucleotide"

BASE COUNT 22 a 14 c 15 g 15 t
 ORIGIN

Query Match 73.3%; Score 48.4; DB 6; Length 66;
 Best Local Similarity 83.3%; Pred. No. 2.1e-07;
 Matches 55; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TCAGATCGATCGCTTGGACAAACGGTAAAGCGGTACGATTCGCTAGCAATT 60
 |||
 DB 1 TCAGATCGATCGCTTGGACAAACGGTAAAGCGGTACGATTCGCTAGCAATT 60

QY 61 CAGCTG 66
 |||
 DB 61 CAGCTG 66

RESULT 4
 AX203113 66 bp DNA linear PAT 30-AUG-2001
 LOCUS AX203113
 DEFINITION Sequence 21 from Patent WO0153502.
 ACCESSION AX203113
 VERSION AX203113.1 GI:15392474
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 AUTHORS Bruce, W.B. and Niu, X.
 TITLE Novel root-preferred promoter elements and methods of use
 JOURNAL Patient: WO 0153502-A 21-JUL-2001;
 PIONEER HI-BRED INTERNATIONAL, INC. (US)
 FEATURES
 source
 1..66
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 20 a 12 c 20 g 14 t 1 others
 ORIGIN

Query Match 57.3%; Score 37.8; DB 6; Length 66;
 Best Local Similarity 73.8%; Pred. No. 0.0018;
 Matches 48; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 GAGATCGATCGCTTGGACAAACGGTAAAGCGGTACGATTCGCTAGCAATT 61
 |||
 DB 2 GAGATCGATCGCTTGGACAAACGGTAAAGCGGTACGATTCGCTAGCAATT 61

QY 62 AGCTG 66
 |||
 DB 62 AGCTG 66

RESULT 5
 AX204093 66 bp DNA linear PAT 30-AUG-2001
 LOCUS AX204093
 DEFINITION Sequence 1 from Patent WO0153502.
 ACCESSION AX204093
 VERSION AX204093.1 GI:15392451
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 AUTHORS Bruce, W.B. and Niu, X.
 TITLE Novel root-preferred promoter elements and methods of use
 JOURNAL Patient: WO 0153502-A 1-JUL-2001;
 PIONEER HI-BRED INTERNATIONAL, INC. (US)
 FEATURES
 source
 1..66
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="random oligonucleotide"

BASE COUNT 19 a 12 c 21 g 14 t
 ORIGIN

Query Match 56.4%; Score 37.2; DB 6; Length 66;
Best Local Similarity 72.7%; Pred. No. 0.003;
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 TGAGATTCGATCCGTTGACAAACGGTAAACCGCTGATTACCGCTACGAATT 60
|||||
DB 1 TGAGATTCGATCCGTTGCGGAGAGGAGGTGAACGACGAATTACCGCTACGAATT 60
|||||

QY 61 CAGCTG 66
|||||

DB 61 CAGCTG 66

RESULT 6
AX203109 66 bp DNA linear PAT 30-AUG-2001
LOCUS
DEFINITION Sequence 17 from Patent W00153502.
ACCESSION AX203109
VERSION AX203109.1 GI:15392470
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 17-26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Source 1..66
/organism="synthetic construct"
/db_xref="taxon:12630"
/note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 19 a 12 c 21 g 14 t

ORIGIN

Query Match 56.4%; Score 37.2; DB 6; Length 66;
Best Local Similarity 72.7%; Pred. No. 0.003;
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 TGAGATTCGATCCGTTGACAAACGGTAAACCGCTGATTACCGCTACGAATT 60
|||||
DB 1 TGAGATTCGATCCGTTGCGGAGAGGAGGTGAACGACGAATTACCGCTACGAATT 60
|||||

QY 61 CAGCTG 66
|||||

DB 61 CAGCTG 66

RESULT 7
AX203110 66 bp DNA linear PAT 30-AUG-2001
LOCUS
DEFINITION Sequence 18 from Patent W00153502.
ACCESSION AX203110
VERSION AX203110.1 GI:15392471
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 18-26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Source 1..66
/organism="synthetic construct"
/db_xref="taxon:12630"
/note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 19 a 12 c 21 g 14 t

ORIGIN

Query Match 56.4%; Score 37.2; DB 6; Length 66;
Best Local Similarity 72.7%; Pred. No. 0.003;
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 TGAGATTCGATCCGTTGACAAACGGTAAACCGCTGATTACCGCTACGAATT 60
|||||
DB 1 TGAGATTCGATCCGTTGCGGAGAGGAGGTGAACGACGAATTACCGCTACGAATT 60
|||||

QY 61 CAGCTG 66
|||||

DB 61 CAGCTG 66

RESULT 8
AX203115 66 bp DNA linear PAT 30-AUG-2001
LOCUS
DEFINITION Sequence 23 from Patent W00153502.
ACCESSION AX203115
VERSION AX203115.1 GI:15392476
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 23-26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Source 1..66
/organism="synthetic construct"
/db_xref="taxon:12630"
/note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 19 a 12 c 22 g 13 t

ORIGIN

Query Match 56.4%; Score 37.2; DB 6; Length 66;
Best Local Similarity 72.7%; Pred. No. 0.003;
Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 TGAGATTCGATCCGTTGACAAACGGTAAACCGCTGATTACCGCTACGAATT 60
|||||
DB 1 TGAGATTCGATCCGTTGCGGAGAGGAGGTGAACGACGAATTACCGCTACGAATT 60
|||||

QY 61 CAGCTG 66
|||||

DB 61 CAGCTG 66

RESULT 9
AX203111 66 bp DNA linear PAT 30-AUG-2001
LOCUS
DEFINITION Sequence 19 from Patent W00153502.
ACCESSION AX203111
VERSION AX203111.1 GI:15392472
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 66)
AUTHORS Bruce, W.B. and Niu, X.
TITLE Novel root-preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 19-26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Source 1..66
/organism="synthetic construct"
/db_xref="taxon:12630"
/note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 19 a 11 c 21 g 14 t 1 others

ORIGIN

ORIGIN

Query Match 54.8%; Score 36.2; DB 6; Length 66;
Best Local Similarity 71.2%; Pred. No. 0.007;
Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 TCAGATTCGATCGCTTCGACAAACGGTAAACGGTACATTCAGCTCTAGCAATT 60
||||| 11111 11111 11111 11111 11111 11111 11111 11111 11111
DB 1 TCAGATTCGATCGCTTCGACAAACGGTAAACGGTACATTCAGCTCTAGCAATT 60
QY 61 CAGCTG 66
|||||
DB 61 CAGCTG 66

RESULT 10
AX203107
LOCUS AX203107 66 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 9 from Patent WO0153502.
ACCESSION AX203107
VERSION AX203107.1 GI:15392460

KEYWORDS

SOURCE
ORGANISM
synthetic construct,
artificial sequence.

REFERENCE
AUTHORS Bruce W.B. and Niu, X.
TITLE Novel tool preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 9 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
LOCATION/Qualifiers

FEATURES

1..66
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
BASE COUNT 7 a 9 c 9 g 11 t 30 others
ORIGIN

Query Match 54.5%; Score 36; DB 6; Length 66;
Best Local Similarity 54.5%; Pred. No. 0.0083;
Matches 36; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TCAGATTCGATCGCTTCGACAAACGGTAAACGGTACATTCAGCTCTAGCAATT 60
||||| 11111 11111 11111 11111 11111 11111 11111 11111 11111
DB 1 TCAGATTCGATCGCTTCGACAAACGGTAAACGGTACATTCAGCTCTAGCAATT 60
QY 61 CAGCTG 66
|||||
DB 61 CAGCTG 66

RESULT 11
AX203107
LOCUS AX203107 66 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 15 from Patent WO0153502.
ACCESSION AX203107
VERSION AX203107.1 GI:15392468

KEYWORDS

SOURCE
ORGANISM
synthetic construct,
artificial sequence.

REFERENCE
AUTHORS Bruce W.B. and Niu, X.
TITLE Novel tool preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 15 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
LOCATION/Qualifiers

1..66
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

BASE COUNT 20 a 12 c 21 g 13 t

ORIGIN

Query Match 53.9%; Score 35.6; DB 6; Length 66;
Best Local Similarity 71.2%; Pred. No. 0.012;
Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 TCAGATTCGATCGCTTCGACAAACGGTAAACGGTACATTCAGCTCTAGCAATT 60
||||| 11111 11111 11111 11111 11111 11111 11111 11111 11111
DB 1 TCAGATTCGATCGCTTCGACAAACGGTAAACGGTACATTCAGCTCTAGCAATT 60
QY 61 CAGCTG 66
|||||
DB 61 CAGCTG 66

RESULT 12
AX203108
LOCUS AX203108 66 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 16 from Patent WO0153502.
ACCESSION AX203108
VERSION AX203108.1 GI:15392469

KEYWORDS

SOURCE
ORGANISM
synthetic construct,
artificial sequence.

REFERENCE
AUTHORS Bruce W.B. and Niu, X.
TITLE Novel tool preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 16 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
LOCATION/Qualifiers

FEATURES

1..66
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
BASE COUNT 19 a 11 c 21 g 15 t
ORIGIN

Query Match 53.9%; Score 35.6; DB 6; Length 66;
Best Local Similarity 71.2%; Pred. No. 0.012;
Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 TCAGATTCGATCGCTTCGACAAACGGTAAACGGTACATTCAGCTCTAGCAATT 60
||||| 11111 11111 11111 11111 11111 11111 11111 11111 11111
DB 1 TCAGATTCGATCGCTTCGACAAACGGTAAACGGTACATTCAGCTCTAGCAATT 60
QY 61 CAGCTG 66
|||||
DB 61 CAGCTG 66

RESULT 13

AX203112
LOCUS AX203112 66 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 20 from Patent WO0153502.
ACCESSION AX203112
VERSION AX203112.1 GI:15392473

KEYWORDS

SOURCE
ORGANISM
synthetic construct,
artificial sequence.

REFERENCE
AUTHORS Bruce W.B. and Niu, X.
TITLE Novel tool preferred promoter elements and methods of use
JOURNAL Patent: WO 0153502-A 20 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
LOCATION/Qualifiers

1..66
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

BASE COUNT 19 a 11 c 21 g 15 t
 ORIGIN

Query Match 53.9% Score 35.6; DB 6; Length 66;
 Best Local Similarity 71.2%; Pred. No. 0.012;
 Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 TGGATCTGGATCGCTTCACAAACGGTAAAGGCGTAGATTACCGCTCAGCAATT 60
 |||||
 Db 1 TGGATCTGGATCGCTTCGGGGAAGGCAAGCTGAAGCAGCAATTACTGCTCAGCAATT 60
 |||||

QY 61 CAGCTG 66
 |||||
 Db 61 CAGCTG 66

RESULT 14
 AX203114 66 bp DNA linear PAT 30-AUG-2001
 DEFINITION Sequence 22 from Patent WO0153502.
 ACCESSION AX203114
 VERSION AX203114.1 GI:15192475
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 synthetic construct.
 TITLE
 AUTHORs Bruce, W.B. and Niu, X.
 JOURNAL Patent: WO 0153502-A 22-26-JUL-2001;
 PIONEER HI-BRED INTERNATIONAL, INC. (US)
 FEATURES
 Location/Qualifiers
 1..66
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="synthetic sequences flanking a random oligonucleotide"

BASE COUNT 19 a 12 c 21 g 13 t 1 others
 ORIGIN

Query Match 52.4% Score 34.6; DB 6; Length 66;
 Best Local Similarity 70.8%; Pred. No. 0.027;
 Matches 46; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 GAGATCTGATCGCTTCGACAAACGGTAAAGCGGTACATTACCGCTCAGCAATT 61
 |||||
 Db 2 GAGATCTGATCGCTTCGGGGAAGGCAAGCTGAAGCAGCAATTACTGCTCAGCAATT 61
 |||||

QY 62 AGCTG 66
 |||||
 Db 62 AGCTG 66

RESULT 15
 AC068959 160666 bp DNA linear HTG 04-JUN-2000
 LOCUS Homo sapiens clone RP11-12010, WORKING DRAFT SEQUENCE, 11 unordered
 DEFINITION pieces.
 ACCESSION AC068959.2 GI:8247876
 VERSION AC068959.2
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 160666)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens clone RP11-12010
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 160666)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F.,
 Boguski, L., Bouckgeater, B., Brown, A., Burkett, G.,

TITLE
 JOURNAL
 COMMENT

Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
 Collamore, A., Cooke, P., Dearellano, K., Dowar, K., Diaz, J. S.,
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
 Galagan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hagos, R., Heaton, A., Horton, L.,
 Howland, J. C., Iliev, I., Johnson, R., Jones, G., Kam, L., Karadas, A.,
 Klein, J., Larocque, K., Lamazares, R., Landers, T., Lechzy, J.,
 Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
 McCarthy, M., McEwan, P., McGuire, A., McInerney, K., McPheters, R.,
 Melarini, J., Menees, L., Mihov, T., Miranda, C., Mienda, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, M., Subramanian, A., Talamas, J.,
 Testage, S., Theodore, J., Tirrell, A., Travers, M., Tsigalou, J.,
 Vassiliev, H., Viel, R., Vo, A., Willison, B., Wu, X., Wyman, D., Ye, W. J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (13-MAY-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 4, 2000 this sequence version replaced gi:7798795.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

 Genomic Center
 Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WMR
 Web site: <http://www.seq.wi.mit.edu>
 Contact: sequence.submissions@genome.wi.mit.edu

 Project Information
 Center project name: L7444
 Center clone name: 12-0-10

 Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 15317 bases at least 940
 Consensus quality: 157272 bases at least 930
 Consensus quality: 156589 bases at least Q20
 Insert size: 163000; agarose-1p
 Insert size: 159666; sum-of-ctigs
 Quality coverage: 4.5 in Q20 bases; agarose-1p
 Quality coverage: 4.6 in Q20 bases; sum-of-ctigs

 NOTE: This is a 'working draft' sequence. It currently
 consists of 11 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1072: contig of 1072 bp in length
 * 1073 1172: gap of 100 bp in length
 * 1173 2585: contig of 1413 bp in length
 * 2586 2685: gap of 100 bp in length
 * 2686 5841: contig of 3156 bp in length
 * 5842 5941: gap of 100 bp in length
 * 5942 16755: contig of 10814 bp in length
 * 16756 16855: gap of 100 bp in length
 * 16856 31901: contig of 15046 bp in length
 * 31902 32001: gap of 100 bp in length
 * 32002 50422: contig of 18421 bp in length
 * 50423 50522: gap of 100 bp in length
 * 50523 67507: contig of 16985 bp in length
 * 67508 67607: gap of 100 bp in length
 * 67608 87476: contig of 19869 bp in length
 * 87477 87576: gap of 100 bp in length
 * 87577 107074: contig of 19498 bp in length
 * 107075 107174: gap of 100 bp in length
 * 107175 132166: contig of 24992 bp in length
 * 132167 132266: gap of 100 bp in length

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FEATURES             * 132267 160666: contig of 28400 bp in length.
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                    /db_xref "taxon:9606"
                    /clone="RP11-12010"
                    /clone_11b="RP11-11 human Male PAC"
                    1..1072
                    /note="assembly_fragment"
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                    vector_side:right"
                    32002..50422
                    /note="assembly_fragment"
                    50523..67507
                    /note="assembly_fragment"
                    67608..87476
                    /note="assembly_fragment"
                    87577..107074
                    /note="assembly_fragment"
                    clone_end:T7
                    vector_side:right"
                    107175..132166
                    /note="assembly_fragment"
                    132267..160666
                    /note="assembly_fragment"
BASE COUNT      51792 a 29540 c 29548 g 48787 t 1009 others
ORIGIN
Query Match      40.3% Score 26.6; DB 2; Length 160666;
Best Local Similarity 64.1%; Pred. No. 45;
Matches 41; Conservative 0; Mismatches 24; Indels 0; Caps 0;
QY      1 TTAGATTGATCGCTGGACAAACGATTAAAAAGCGTACATTACGCTCAGCAATT 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      8413 TGTGATTTGTTGCTGATCAAGTTTATATAAAGTAAGCTTATCTCCACCTAATA 8354
QY      61 CAGCTT 65
      |||||
DB      8353 CAGAT 8349

```

Search completed: November 5, 2002, 06:26:38
 Job time : 358.568 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

(M) nucleic - nucleic search, using sw model

Run on: November 5, 2002, 05:25:34 : Search time 95.9421 Seconds

(without alignments)
1181.091 Million cell updates/sec

Title: US-09-766-113-2

Perfect score: 66
Sequence: 1 ttaatctgcatcgttcca.....cgtctcagatcagctg 66

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

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2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

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23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	66	22	AAS08433
2	66	100.0	66	22	AAS08453
3	48.4	73.3	66	22	AAS08434
4	37.8	57.3	66	22	AAS08450
5	37.2	56.4	66	22	AAS08432
6	37.2	56.4	66	22	AAS08452
7	36.2	54.8	66	22	AAS08448
8	36	54.5	66	22	AAS08440
9	35.6	53.9	66	22	AAS08446

10	35.6	53.9	66	22	AAS08447	A plant root-prete
11	35.6	53.9	66	22	AAS08449	A plant root-prete
12	34.6	52.4	66	22	AAS08451	A plant root-prete
13	26	39.4	26	22	AAH42733	A promoter element
14	26	39.4	3181	18	AAV74611	Staphylococcus aur
15	25.2	38.2	65	22	AAS08445	A plant root-prete
16	25.2	38.2	4157	23	AB1068435	Drosophila melanog
17	25.2	38.2	8011	23	AB106834	Drosophila melanog
18	24.4	37.0	816	22	AAH33570	S. epidermidis ope
19	24.4	37.0	1263	23	AAH73285	DNA encoding novel
20	24.4	37.0	1263	22	AAH81874	DNA encoding novel
21	24.4	37.0	3229	22	AAH54503	S. epidermidis gen
22	24.4	37.0	3300	21	AAZ55699	DNA encoding yeast
23	24.2	36.7	2290	19	AAV43879	Mycobacterium meth
24	24.2	36.7	5894	23	AB118043	Drosophila melanog
25	24.2	36.7	12245	23	AB118042	Drosophila melanog
26	24.2	36.7	4403765	22	AA199683	Mycobacterium tube
27	24	36.4	62	22	AAS08437	A plant root-prete
28	23.8	36.1	13549	23	AB107964	Drosophila melanog
29	23.6	35.8	2524	23	AAH70677	DNA encoding novel
30	23.6	35.8	2886	23	AAH79513	DNA encoding novel
31	23.6	35.8	3804	23	AAH70040	DNA encoding novel
32	23.6	35.8	15387	24	AB132184	Human immune syste
33	23.4	35.5	419	21	AAH94671	Cat flea hindgut a
34	23.2	35.2	64	22	AAH08439	A plant root-prete
35	23.2	35.2	9676	23	AB109554	Drosophila melanog
36	23.2	35.2	27671	21	AAH81474	N. meningitidis pa
37	23.2	35.2	349980	21	AAH21611	Neisseria meningit
38	23.2	35.2	837096	21	AAH1489	N. meningitidis pa
39	23	34.8	6069	24	AAH61380	Human gene regulat
40	23	34.8	47066	23	AB111514	Drosophila melanog
41	22.4	33.9	245	21	AAH01453	Human colon cancer
42	22.4	33.9	369	23	AAH81849	DNA encoding novel
43	22.4	33.9	793	23	AAH69854	DNA encoding novel
44	22.4	33.9	1168	22	AAH60852	Pseudomonas sp exp
45	22.4	33.9	1861	20	AAH04212	pAP-222 insert con

ALIGNMENTS

RESULT 1	
AAS08433	
ID	AAS08433 standard; DNA: 66 BP.
XX	
AC	AAS08433;
XX	
DT	26-SFP-2001 (first entry)
XX	
DE	A plant root-preferred promoter element (RPE), RPE 14.
XX	
KW	Root-preferred promoter element; RPE; abiotic stress; drought;
KW	salinity; pesticide resistance; herbicide resistance; biotic stress;
KW	disease resistance; fungal disease; bacterial disease; viral disease;
KW	insect attack; nematode attack; RPE14; random oligonucleotide library;
OS	ROL; ss.
XX	
OS	Synthetic.
XX	
EH	
FT	Key
FT	misc_feature
FT	location/qualifiers
FT	1..18
FT	/tag- a
FT	/label= "5'_flanking_sequence"
FT	19..48
FT	/tag- b
FT	/note= "Randomised sequence"
FT	49..66
FT	/tag- c
FT	/label= "3'_flanking_sequence"
XX	
PN	W0200153502-A2.
XX	
PD	26-JUL-2001.

FIGURE 6 | The sequence representation of plant root-preferred promoter elements RPEs isolated from a random oligonucleotide library (ROL). The invention concerns a method of identifying and isolating tissue-preferred promoter elements comprising the use of a mixture or random oligonucleotides, flanked by 5' and 3' flanking sequences, which hybridise to tissue-specific plant nuclear proteins, isolating the complexes and PCR amplifying the band oligonucleotide. The method is used for isolating tissue-specific promoters from plants, including but not limited to rice. Rice specific promoters or root preferred promoter elements (RPE) are linked to a nucleotide sequence whose expression is to be controlled to achieve a desired phenotypic effect, e.g., abiotic stress (drought, temperature, salinity, pesticide and herbicide resistance), biotic stress (disease resistance, nematode attack, resistance to attack by fungi, bacteria, viruses, insects and nematodes).

Sequence: 66 BP; 21 A; 14 C; 16 G; 15 T; 0 other;

Query Match: 100.0%; Score: 66; DB: 22; Length: 66;
Host: Local Similarity: 100.0%; Proc. No.: 2,7e-16;
Matches: 66; Conservative: 0; Mismatches: 0; Indels: 0; Caps: 0.

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|||||
B 1 TGAATCTTGAGATTCGTCCACAAAGAAGTAATAAAAGCGCATACGCCTCACCAATT 60
|||||
G 61 CAAGTCG 66
|||||
D 61 CAAGTCG 66

RESULT 2

AAS0845_1
ID: AAS0845_1 Standard; DNA; 66 BP.
AC: AAS0845_1;
XX
XX
XX 26-SEP-2001 (first entry)
XX
DE A Plant root preferred promoter element (RPE); RPE 21.
XX
XX Root preferred promoter element; RPE: abiotic stress; drought;
XX saltinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE21: Random oligonucleotide library;
XX Roll; ss.
XX
XX Synthesis:
XX
XX Key Location/Qualifiers
FH Locus_tag = 1..JB
FT misc_feature /start = 4
FT misc_feature /label = "5'_flanking_sequence"
FT misc_feature 19..48
FT /start = b
FT /note = "Randomised sequence"

ET	misfeature	49..66	
ET		/star	"3'_flanking_sequence"
XX			
EN	W200154502-A2.		
XX			
ED	26-JUL-2001.		
XX			
ED	19-JAN-2001; 2001W0-US02011.		
XX			
ED	21-JAN-2000; 2000US-0177473.		
XX			
EA	(P10N-) PIONEER HI-BRED INT INC.		
XX			
P1	Bruce WB, Niu X:		
XX			
DR	WPI: 2001-442261/47.		
XX			
ET	producing tissue-preferred promoter elements constructs for regulating		
ET	expression of nucleotide sequences in a plant comprises identifying and		
ET	isolating tissue-preferred promoter elements -		
XX			
PS	Example 1: Fig 1; 45pp; English.		
XX			
CC	The sequence represents a plant root-preferred promoter element, RPE,		
CC	isolated from a random oligonucleotide library (ROL). The invention		
CC	comprises a method of identifying and isolating tissue-preferred promoter		
CC	elements comprising the use of a mixture of random oligonucleotides,		
CC	labeled by 5' and 3' flanking sequences, isolating the complexes and PCR		
CC	specifically the bound oligonucleotide. The method is used for isolating		
CC	amplifying the bound oligonucleotide. The method is used for isolating		
CC	tissue specific promoters from plants, including but not limited to		
CC	root-specific promoters or root-preferred promoter elements (RPE). The		
CC	RPEs are useful in the genetic manipulation of a plant when operably		
CC	linked to a nucleotide sequence whose expression is to be controlled to		
CC	achieve a desired phenotypic effect, e.g. abiotic stress (drought,		
CC	temperature, salinity, pesticide and herbicide resistance) and biotic		
CC	stress (disease resistance, resistance to attack by fungi, bacteria,		
CC	viruses, insects and nematodes).		
XX			
SD	Sequence 66 BP: 21 A; 14 C; 16 G; 15 T; 0 other;		
XX			
Query Match	100.0%; Score 66; DR 22; Length 66;		
Best Local Similarity	100.0%; Preq. No. 2.7e-16;		
Matches	66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 TGAGATGTGATCGCTTCGACAAACGTAATAATACCGTCTACGAAAT 60		
DB	1 TGAAGTCTGATCGCTTCGACAAACGTAATAATACCGTCTACGAAAT 60		
QY	61 CAGCTG 66		
DB	61 CAGCTG 66		
XX			
RESULT 3			
AA08434	standard; DNA; 66 BP.		
XX			
AC	AA08434:		
XX			
DT	26-SEP-2001 (first entry)		
XX			
DE	A plant root-preferred promoter element (RPE), RPE 19.		
XX			
XX	Root-preferred promoter element; RPE; abiotic stress; drought;		
KM	salinity; pesticide resistance; herbicide resistance; biotic stress;		
XX	disease resistance; fungal disease; bacterial disease; viral disease;		
KM	insect attack; nematode attack; RPE19; random oligonucleotide library;		
XX	ROL; SS.		
XX			
XX	Synthetic.		

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FT		/tag= 4
FT	misc_feature	/label= "5'-flanking_sequence"
FT		19..48
FT		/tag= b
FT	misc_feature	/note= "Randomised sequence"
FT		49..66
FT		/tag= c
FT		/label= "3'-flanking_sequence"
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XX		W6200153f02.A2.
XX		26-JUL-2001.
XX		
PF		19-JAN-2001; 2001WO-US02011.
XX		
PR		21-JAN-2000; 2000US-O177473.
XX		
PA	(PION-) PIONEER HI-BRED INT INC.	
P1	Bruce WB, Niu X;	
XX		
DR	WP1: 2001-442261/47.	
XX		
PT	Production tissue-preferred promoter elements constructs for regulating expression of nucleotide sequences in a plant comprises identifying and isolating tissue-preferred promoter elements -	
PS	Claim 5; Fig 1; 45pp: English.	
XX		
CC	The sequence represents a plant root-preferred promoter element, RPE,	
CC	isolated from a random oligonucleotide library (ROL). The invention	
CC	concerns a method of identifying and isolating tissue-preferred promoter	
CC	elements comprising the use of a mixture of random oligonucleotides,	
CC	flanked by 5' and 3' flanking sequences, which hybridize to tissue-	
CC	-specific plant nuclear proteins, isolating the complexes and PCR	
CC	amplifying the bound oligonucleotide. The method is used for isolating	
CC	tissue-specific promoters from plants, including but not limited to	
CC	root-specific promoters or root-preferred promoter elements (RPE). The	
CC	RPEs are useful in the genetic manipulation of a plant when operably	
CC	linked to a nucleotide sequence whose expression is to be controlled to	
CC	achieve a desired phenotypic effect, e.g., abiotic stress (drought,	
CC	temperature, salinity, pesticide and herbicide resistance) and biotic	
CC	stress (disease resistance, resistance to attack by fungi, bacteria,	
CC	viruses, insects and nematodes).	
XX		
SQ	Sequence 66 BP; 22 A; 14 C; 15 G; 15 T; 0 other:	
	Query Match: 73.3%; Score 48.4; DR 22; Length 66;	
	Host Local Similarity 83.3%; Pied. No. 2e-09;	
	Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0	
ZY	I GAGATGTCATCGCTTCCACAAAGGTAAAAAGCGGTACATTACGGCTGCATT 60	
DB	I TGACATCTGATCGCTTCCACAAAACGGTAATAACTAAAGTAAGTGACGTTCAAGATT 60	
QY	61 CAGCTG 66	
DB	61 CAGCTG 66	
RESULT 4		
AAS08450		
ID	AAS08450 standard; DNA: 66 BP.	
XX	AAS08450;	
XX	26-SEP-2001 (first entry)	
DE	A plant root-preferred promoter element (RPE), RPE 33.	
XX		
KX	Root-preferred promoter element; RPE; abiotic stress; drought;	

```

KW salinity, pesticide resistance, herbicide resistance, biotic stress;
KW disease resistance, fungal disease, bacterial disease, viral disease;
KW insect attack, nematode attack; RPFs: random oligonucleotide library;
KW ROL: ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1..18 /*tag= a
FH misc_feature misc_feature
FH 19..48 /label= "5'-flanking-sequence"
FH misc_feature 19..48
FH /*tag= b
FH /note= "Randomised sequence"
FH misc_feature 49..66
FH /*tag= c
FH 73..77 /label= "3'-flanking-sequence"
XX
XX W0200153502-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-0502011.
XX
XX 21-JAN-2000; 2000US-0177473.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X;
XX
XX WPI: 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprising identifying and
XX isolating tissue-preferred promoter elements.
XX
XX Example 1: Fig 1: 45pp: English.
XX
XX The sequence represents a plant root-preferred promoter element, RPF,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 66 BP: 20 A; 12 C; 20 G; 13 T; 1 other:
XX
XX Query Match 57.8%; Score 37.8; DB 22; Length 66;
XX Best Local Similarity 73.8%; Pred. No. 2.7e-05;
XX Matches 48; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
XX
XX 2 GAGAGTCGATCGCTTCGATGAAGAAACCGTAAAGAACGGGTACATTCAGCTCTACGAATTC 61
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 2 GAGAGTCGATCGCTTCGAGGAAAGGGAAGCTGAAAGCAAAATTAACGCTCTACGAATTC 61
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX
XX 62 AGCTG 66
XX | | | |
XX 62 AGCTG 66
XX
XX RESULT 5
XX AAS08432
XX ID AAS08432 standard; DNA: 66 BP.
XX

```

```

AC AAS08452:
XX
DE 26-SEP-2001 (first entry)
XX
XX A plant root-preferred promoter element (RPE), RPE 15.
XX
XX Root preferred promoter element: RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE15; random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX
XX Key location/qualifiers
XX misc_feature /tag= a
XX /label= "5'_flanking_sequence"
XX /tag= b
XX /note= "Randomised sequence"
XX misc_feature /tag= c
XX /label= "3'_flanking_sequence"
XX
XX W0200154502-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-0502011.
XX
XX 21-JAN-2000; 2000US-0177473.
XX
XX (PION ) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X;
XX
XX WP1: 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements -
XX
XX Claim 5; Fig 1; 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins; isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stresses (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 66 BP; 19 A; 12 C; 21 G; 14 T; 0 other;
XX
XX Query Match 56.4%; Score 37.2; DB 22; Length 66;
XX Best Local Similarity 72.7%; Pred. No. 4.6e-05;
XX Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX
XX 1 TGGAGTCTGATCGCTGGCAAAAGCGTATTAATTCCTGCTACCAATT 60
XX |
XX 1 TGGAGTCTGATCGCTGGCGAAGGAGAGCTGAACGCAACATTACCGCTACCAANT 60
XX |
XX 61 CAGCTG 66
XX |
XX

```

```

DB 61 CAGCTG 66
XX
XX RESULT 6
XX AAS08452
XX ID AAS08452 standard; DNA; 66 BP.
XX
XX AAS08452:
XX
XX 26-SEP-2001 (first entry)
XX
XX A plant root-preferred promoter element (RPE), RPE 73.
XX
XX Root-preferred promoter element: RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE73; random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX
XX Key location/qualifiers
XX misc_feature /tag= a
XX /label= "5'_flanking_sequence"
XX /tag= b
XX /note= "Randomised sequence"
XX misc_feature /tag= c
XX /label= "3'_flanking_sequence"
XX
XX W0200154502-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-0502011.
XX
XX 21-JAN-2000; 2000US-0177473.
XX
XX (PION ) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X;
XX
XX WP1: 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements -
XX
XX Example 1; Fig 1; 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins; isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stresses (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
XX Sequence 66 BP; 19 A; 12 C; 22 G; 14 T; 0 other;
XX
XX Query Match 56.4%; Score 37.2; DB 22; Length 66;
XX Best Local Similarity 72.7%; Pred. No. 4.6e-05;
XX Matches 48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX

```

```

QY 1 TCGATGTCGATCGGTGACGAAAAAGCGTAAAAAGCGGTACGATTCGATGCAATT 60
DB 1 TGAAGATCTGATCGGTTCGAGAAAGCGAAGCTGAAGGCGAGAGAAATACGTCTGACGATT 60
QY 63 CAGCTG 66
DB 61 CAGCTG 66
111111
RESULT 7
1E AAS084448 AAS084448 standard; DNA: 66 BP.
XX
XX AAS084448:
XX
XX 26-SEP-2001 (first entry)
DE
XX A plant root-preferred promoter element (RPE), RPE 89.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
KW salinity; pesticide resistance; herbicide resistance; biotic stress;
KW disease resistance; fungal disease; bacterial disease; viral disease;
KW insect attack; nematode attack; RP89; random oligonucleotide library;
KW ROL; SS.
XX
XX Synthetic.
XX
XX Key location/Qualifiers
XX misc_feature 1..18
XX /tag= a
XX /label= "5'_flanking_sequence"
XX misc_feature 19..48
XX /tag= b
XX /note= "Randomised sequence"
XX misc_feature 49..66
XX /tag= c
XX /label= "3'__flanking_sequence"
XX
XX W0200153502-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001: 2001WO-US02011.
XX
XX 21-JAN-2000: 2000US-0177473.
XX
XX (P10N-) PIONEER HI-BRED INT. INC.
XX
XX Bruce WB, Niu X:
XX
XX WPI: 2001-442261/47.
XX
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance), resistance to attack by fungi, bacteria,

```

CC	viruses, insects and nematodes).
XX	
SO	Sequence 66 BP; 19 A; 11 C; 21 G; 14 T; 1 other:
	Query Match 54.8%; Score 36.2; DB 22; Length 66;
	Best Local Similarity 71.2%; Pred. No. 0.00011;
	Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY	1 TGACATCTGATCGCTTCGACCAACGCTAAACGCGTACGATTCGCTCTAGCAATT 60
DB	1 TGCATCTGATCTGATCTGCTTCGCGACAGCGAAGCTGAAACGACGATACGCTCTACCAATT 60
OY	61 CAGCTG 66
DB	61 CAGCTG 66
RESULT 8	
AA080440	
ID	AA080440 standard; DNA: 66 BP.
AC	
XX	AA080440;
XX	
DT	26-SEP-2001 (first entry)
XX	
DE	A random oligonucleotide library, ROL, sequence n19813.
XX	
KM	Root-preferred promoter element; RPE: abiotic stress; drought;
KM	salinity; pesticide resistance; herbicide resistance; biotic stress;
KM	disease resistance; fungal disease; bacterial disease; viral disease;
KW	insect attack; nematode attack; random oligonucleotide library;
KW	ROL; n19813; ss.
XX	
OS	Synthetic.
XX	
EH	Key
ET	Location/Qualifiers
ET	misc_feature 1..18
ET	/tag= a
ET	/label= "5'_flanking_sequence"
ET	19..48
ET	/tag= b
ET	misc_feature 49..66
ET	/note= "Randomised sequence"
ET	49..66
ET	/tag= c
ET	/label= "3'_flanking_sequence"
XX	
PN	W0200153502-A2.
XX	
PD	26-JUL-2001.
XX	
PF	19-JAN-2001; 2001MO-US02011.
XX	
PE	21-JAN-2000; 2000US-0177473.
XX	
PA	(PION-) PIONEER HI-BRED INT INC.
XX	
PI	Bruce WR, Niu X;
XX	
DR	WPI: 2001-442261/47.
XX	
PT	Producing tissue-preferred promoter elements constructs for regulating
PT	expression of nucleotide sequences in a plant comprises identifying and
PT	isolating tissue-preferred promoter elements -
XX	
PS	Example 1: Page 21; 45pp; English.
XX	
CC	The sequence represents a random oligonucleotide library (ROL) construct
CC	used to isolate tissue-specific promoter elements. The invention
CC	concerns a method of identifying and isolating tissue-preferred promoter
CC	elements comprising the use of a mixture of random oligonucleotides,
CC	flanked by 5' and 3' flanking sequences, which hybridise to tissue-
CC	specific plant proteins, isolating the complexes and PCR
CC	amplifying the bound oligonucleotide. The method is used for isolating

```
CC Tissue-specific promoters from plants, including but not limited to
CC root specific promoters or root-preferred promoter elements (RPE). The
CC RPEs are useful in the genetic manipulation of a plant when operably
CC linked to a nucleotide sequence whose expression is to be controlled to
CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
CC temperature, salinity, pesticide and herbicide resistance) and biotic
CC stress (disease resistance, resistance to attack by fungi, bacteria,
CC viruses, insects and nematodes).
XX
SU Sequence 66 BP; 7 A; 9 C; 9 G; 11 T; 30 other;
Query Match 54.5%; Score 16; DR 22; Length 66;
Best Local Similarity 54.5%; Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
GY 1 TGAATCTGATCCCTTCGCAAAACGCTAAACAGCTAGCATCTCTAGCAATT 60
DB 1 TGAATCTGATCCCTTCGCAAAACGCTAAACAGCTAGCATCTCTAGCAATT 60
GY 61 CAGCTG 66
DB 61 CAGCTG 66
RESULT 9
AAS08446
ID AAS08446 standard; DNA; 66 BP.
AC AAS08446;
DE 26-SEP-2001 (first entry)
XX
DE A plant root-preferred promoter element (RPE); RPE 18.
XX
KM Root-preferred promoter element; RPE; abiotic stress; drought;
KM salinity; pesticide resistance; herbicide resistance; biotic stress;
KM disease resistance; fungal disease; bacterial disease; viral disease;
KM insect attack; nematode attack; RPE18; random oligonucleotide library;
KM ROL; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..18 /tag a
FT /label "5' flanking_sequence"
FT misc_feature 19..48 /tag b
FT /note "Randomised sequence"
FT misc_feature 49..66 /tag c
FT /label "3' flanking_sequence"
XX
PN W0200154502-A2.
XX
PD 26-JUL-2001.
XX
PE 19-JAN-2001; 2001WO-0502011.
XX
PR 21-JAN-2000; 2000US-0177473.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Bruce WB, Niu X;
XX
DB WPI: 2001-442261/47.
XX
PT Production tissue preferred promoter elements constructs for regulating
PT expression of nucleotide sequences in a plant comprises identifying and
PT isolating tissue preferred promoter elements -
XX
PS Example 1: Fig 1: 45pp; English.
XX
```

```
CC The sequence represents a plant root-preferred promoter element, RPE,
CC isolated from a random oligonucleotide library (ROL). The invention
CC concerns a method of identifying and isolating tissue-preferred promoter
CC elements comprising the use of a mixture of random oligonucleotides,
CC flanked by 5' and 3' flanking sequences, which hybridize to tissue-
CC specific plant nuclear proteins, isolating the complexes and PCR
CC amplifying the bound oligonucleotide. The method is used for isolating
CC tissue-specific promoters from plants, including but not limited to
CC root-specific promoters or root-preferred promoter elements (RPE). The
CC RPEs are useful in the genetic manipulation of a plant when operably
CC linked to a nucleotide sequence whose expression is to be controlled to
CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
CC temperature, salinity, pesticide and herbicide resistance) and biotic
CC stress (disease resistance, resistance to attack by fungi, bacteria,
CC viruses, insects and nematodes).
XX
SU Sequence 66 BP; 20 A; 12 C; 21 G; 13 T; 0 other;
Query Match 54.9%; Score 15.6; DR 22; Length 66;
Best Local Similarity 71.2%; Pred. No. 0.00019;
Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
GY 1 TGAATCTGATCCCTTCGCAAAACGCTAAACAGCTAGCATCTCTAGCAATT 60
DB 1 TGAATCTGATCCCTTCGCAAAACGCTAAACAGCTAGCATCTCTAGCAATT 60
GY 61 CAGCTG 66
DB 61 CAGCTG 66
RESULT 10
AAS08447
ID AAS08447 standard; DNA; 66 BP.
AC AAS08447;
DE 26-SEP-2001 (first entry)
XX
DE A plant root-preferred promoter element (RPE); RPE 32.
XX
KM Root-preferred promoter element; RPE; abiotic stress; drought;
KM salinity; pesticide resistance; herbicide resistance; biotic stress;
KM disease resistance; fungal disease; bacterial disease; viral disease;
KM insect attack; nematode attack; RPE32; random oligonucleotide library;
KM ROL; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..18 /tag a
FT /label "5' flanking_sequence"
FT misc_feature 19..48 /tag b
FT /note "Randomised sequence"
FT misc_feature 49..66 /tag c
FT /label "3' flanking_sequence"
XX
PN W0200154502-A2.
XX
PD 26-JUL-2001.
XX
PE 19-JAN-2001; 2001WO-0502011.
XX
PR 21-JAN-2000; 2000US-0177473.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Bruce WB, Niu X;
XX
DB WPI: 2001-442261/47.
XX
```

[illegible]

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PR 21-JAN-2000; 2000US-0177473.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X:
XX
XX WP1: 2001-442201/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
PT expression of nucleotide sequences in a plant comprises identifying and
PT isolating tissue-preferred promoter elements.
XX
XX
XX Example 1: Fig 1: 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
CC isolated from a random oligonucleotide library (ROL). The invention
CC concerns a method of identifying and isolating tissue-preferred promoter
CC elements comprising the use of a mixture of random oligonucleotides,
CC flanked by 5' and 3' flanking sequences, which hybridise to tissue-
CC specific plant nuclear proteins, isolating the complexes and PCR
CC amplifying the bound oligonucleotide. The method is used for isolating
CC tissue-specific promoters or root promoters, including but not limited to
CC root-specific promoters or root-preferred promoter elements (RPE). The
CC RPEs are useful in the genetic manipulation of a plant when operably
CC linked to a nucleotide sequence whose expression is to be controlled to
CC achieve a desired phenotypic effect, e.g. abiotic stress (drought,
CC temperature, salinity, pesticide and herbicide resistance) and biotic
CC stress (disease resistance, resistance to attack by fungi, bacteria,
CC viruses, insects and nematodes).
XX
XX
XX Sequence 66 BP: 19 A; 11 G; 21 G; 15 T; 0 other;
SQ
XX
XX
XX Query Match 53.9%; Score 35.6; DH 22; Length 66;
XX Best Local Similarity 71.2%; Pred. No. 0.00019;
XX Matches 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
XX
XX 1 TGACATCTGATCGTTCGACAAACGGGTAAACCGGTACATTACCTGCTACGCAATT 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 1 TGAATCTGTGATCGTTCGCGGAGAGGGAAGGTGAACGCAAGCAATTACTTCTACGCAATT 60
XX
XX
XX 61 CACGCTG 66
XX | | | | |
XX 61 CACGCTG 66
XX
XX
XX RESULT 12
XX AAS08451
XX ID AAS08451 standard; DNA; 66 BP.
XX
XX AAS08451:
XX
XX 26-SEP-2001 (first entry)
XX
XX A plant root-preferred promoter element (RPE), RPE 71.
XX
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE71; random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1..18
XX FT /label= "5'_flanking_sequence"
XX FT misc_feature 19..48
XX FT /tag= b
XX FT /note= "Randomised sequence"
XX FT misc_feature 49..66
XX FT /tag= c
XX FT /label= "3'_flanking_sequence"
XX

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XX	W0200154502-A2.
XX	
XX	26_JUL_2001.
XX	
XX	19-JAN-2001: 2001W0-US02011.
XX	
XX	21 JAN 2000: 2000US-0177473.
XX	
XX	(PION-) PIONEER III-BRED INT INC.
XX	
XX	BRUCE WB, Niu X;
XX	
XX	WPI: 2001-442261/47.
XX	
XX	Example 1; Fig 1; 45pp; English.
XX	
XX	The sequence represents a plant root-preferred promoter element, RPE,
XX	isolated from a random oligonucleotide library (ROL). The invention
XX	concerns a method of identifying and isolating tissue-preferred promoter
XX	elements comprising the use of a mixture of random oligonucleotides,
XX	labeled by 5' and 3' flanking sequences, which hybridize to tissue-
XX	specific plant nuclear proteins, isolating the complexes and PCR
XX	amplifying the bound oligonucleotide. The method is used for isolating
XX	tissue-specific promoters from plants, including but not limited to
XX	roots. RPEs are useful in the genetic manipulation of a plant when operably
XX	linked to a nucleotide sequence whose expression is to be controlled to
XX	achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX	temperature, salinity, pesticide and herbicide resistance) and biotic
XX	stress (disease resistance, resistance to attack by fungi, bacteria,
XX	viruses, insects and nematodes).
XX	
XX	Sequence 66 BP; 19 A; 12 G; 21 C; 13 T; 1 other;
XX	
XX	Query Match 52.4%; Score 34.6; DB 22; Length 66;
XX	Best Local Similarity 70.8%; Pred. No. 0.00048;
XX	Matches 46; Conservative 0; Mismatches 19; Indels 0; Gaps
XX	0;
XX	
XX	2 GAGCTGCGATCGCTTGATCAAAACGCGTAAAAAATCGGTACATTCGCTGTAGCAATTC 61
XX	
XX	2 GAGCTGCGATCGCTTGCTGGCGGAGGAGGAGGATCAAGTAAAGTAAAGATTACTCTCTAGCAATTC 61
XX	
XX	62 AGTTG 66
XX	
XX	62 AGTTG 66
XX	
XX	RESULT 14
XX	AAH42734
XX	AAH42734 standard; DNA; 26 BP.
XX	
XX	AAH42734:
XX	
XX	01-OCT-2001 (first entry)
XX	
XX	A promoter element or transcription binding site.
XX	
XX	Promoter element; transcription binding site; plant promoter; SDRP;
XX	synthetic multimeric promoter element region; gene expression;
XX	insect resistance; herbicide resistance; ss.
XX	
XX	Synthetic.
XX	
XX	W0200154476-A2.
XX	
XX	26-JUL_2001.
XX	
XX	19-JAN-2001: 2001W0-US02024.

XX	21-JAN-2000; 20000S-0177437.
PR	(PION-) PIONEER HI-BRED INT INC.
XX	
XX	Bruce WB, Niu X:
XX	WP1; 2001-476118/51.
XX	
XX	New plant promoters with synthetic multimeric promoter regions,
PT	useful in plant molecular biology, particularly in regulating gene
PT	expression in plants to increase resistance against insects or
PT	herbivores.
XX	
XX	Example 1; Fig 1; 67pp; English.
XX	
XX	AAH42709-72 represent promoter elements or transcription binding sites.
CC	regions are used to construct synthetic multimeric promoter element
CC	regions (SMERS). The specification describes plant promoters which
CC	comprise SMERS. The plant promoters are useful in plant molecular
CC	biology, particularly in regulating gene expression in plants. The
CC	promoters are especially useful for transforming plants or plant cells,
CC	e.g. to increase resistance against insects or herbivores.
XX	
XX	Sequence 26 BP; 12 A; 4 C; 6 G; 4 T; 0 other;
XX	
XX	Query Match 39.4%; Score 26; 08 22; Length 26;
XX	Post Local Similarity 100.0%; Pct. No. 0.87;
XX	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	23 AACGGTAAAAAGCGTAGATTACC 48
DB	1 AACCGTAAAAAGCGTAGATTACC 26
XX	
XX	RESULT 14
ID	AAV74611
XX	AAV74611 standard; DNA; 3181 BP.
XX	AAV74611;
XX	
XX	16-MAR-1999 (first entry)
DT	
XX	
XX	Staphylococcus aureus contig SF01 ID #100.
DE	
XX	
XX	Computer readable medium; vaccine; S. aureus infection; immunodetection;
KM	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KM	skin infection; surgical wound infection; scalded skin syndrome;
KM	toxic shock syndrome; ds.
XX	
XX	Staphylococcus aureus.
OS	
XX	
XX	Key Location/Qualifiers
FH	
FT	misc_feature 181..240
FT	/*tag= a
FT	/note= "these bases represent a line of missing text in
FT	the sequence listing in the specification, they
FT	are included to maintain the nucleotide numbering
FT	given in the specification for this DNA sequence"
FT	misc_feature 181..2040
FT	/*tag= b
FT	/note= "these bases represent a line of missing text in
FT	the sequence listing in the specification, they
FT	are included to maintain the nucleotide numbering
FT	given in the specification for this DNA sequence"
XX	
XX	FP786519-A2.
PN	
XX	
XX	30-JUL-1997.
PD	
XX	
XX	07-JAN-1997; 97EP-0100117.
PF	
XX	
XX	96US-0009861.
PR	

```

XX (HUMA-) HUMAN GENOME SCI INC.
XX Barash SC, Choi GH, Dillon FJ, Fannon MR, Kunsch CA:
P1 Rosen CA:
XX WPI: 1997-374922/35.
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus
P1 stored on computer readable medium and used in the production of
P1 anti-S.aureus vaccines
XX
XX Claim 1: Page 1128-1130; 3271pp; English.
XX
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.
XX
S0 Sequence 3181 BP; 1005 A; 549 C; 483 G; 1022 T; 122 other:
XX
Query Match 39.4%; Score 26; DB 18; Length 3181;
Best Local Similarity 62.1%; Pred. No. 2.6;
Matches 41; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
XX
QY 1 TGACATCTGCATCGTTCGACAAACGTAATAAACGCGTACGCTACGCAATT 60
DB 1134 TAAATATGACACCATTAATTGTTTACAGCATTAATACCTAAATAAG 1193
XX
QY 61 CAGCTG 66
DB 1194 CAGCTG 1199
XX
RESULT 15
AAS08445
ID AAS08445 standard; DNA: 65 BP.
AC AAS08445;
XX
XX 26-SEP-2001 (first entry)
XX
DE A plant root-preferred promoter element (RPE), RPE 5.
XX
XX Root-preferred promoter element; RPE; abiotic stress; drought;
XX salinity; pesticide resistance; herbicide resistance; biotic stress;
XX disease resistance; fungal disease; bacterial disease; viral disease;
XX insect attack; nematode attack; RPE5; random oligonucleotide library;
XX ROL; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..18
XX /tag: a
XX /label= "5'_flanking_sequence"
XX misc_feature 19..47
XX /tag: b
XX /note= "Randomised sequence"
XX
FT

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FT misc_feature 48..65
FT /tag: c
FT /label= "3'_flanking_sequence"
XX
XX W0200153502-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001W0-US02011.
XX
XX 21-JAN-2000; 2000US-0177473.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Bruce WB, Niu X:
XX
XX WPI: 2001-442261/47.
XX
XX Producing tissue-preferred promoter elements constructs for regulating
XX expression of nucleotide sequences in a plant comprises identifying and
XX isolating tissue-preferred promoter elements -
XX
XX Example 1: Fig 1; 45pp; English.
XX
XX The sequence represents a plant root-preferred promoter element, RPE,
XX isolated from a random oligonucleotide library (ROL). The invention
XX concerns a method of identifying and isolating tissue-preferred promoter
XX elements comprising the use of a mixture of random oligonucleotides,
XX flanked by 5' and 3' flanking sequences, which hybridise to tissue-
XX specific plant nuclear proteins, isolating the complexes and PCR
XX amplifying the bound oligonucleotide. The method is used for isolating
XX tissue-specific promoters from plants, including but not limited to
XX root-specific promoters or root-preferred promoter elements (RPE). The
XX RPEs are useful in the genetic manipulation of a plant when operably
XX linked to a nucleotide sequence whose expression is to be controlled to
XX achieve a desired phenotypic effect, e.g. abiotic stress (drought,
XX temperature, salinity, pesticide and herbicide resistance) and biotic
XX stress (disease resistance, resistance to attack by fungi, bacteria,
XX viruses, insects and nematodes).
XX
S0 Sequence 65 BP; 18 A; 14 C; 17 G; 16 T; 0 other:
XX
Query Match 38.2%; Score 25.2; DB 22; Length 65;
Best Local Similarity 71.2%; Pred. No. 2.2;
Matches 47; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
XX
QY 1 TGACATCTGCATCGTTCGACAAACGTAATAAACGCGTACGCTACGCAATT 60
DB 1 TCGATCTGCATCGTTCGACGACGTAATAAGTAAGCAAGCGCCGCTT TCGTCTACGCAATT 59
XX
QY 61 CAGCTG 66
DB 60 CAGCTG 65
XX
Search completed: November 5, 2002. 05:41:46
Job time : 100.942 secs

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GenCore version 5.1.3
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UM nucleic - nucleic search, using sw model

Run on: November 5, 2002, 05:26:39 : Search time 22.2973 seconds
(without alignments)
727.075 Million cell updates/sec

Title: US-09-766-113-2
Perfect score: 66
Sequence: 1 tgaatcgcgacccatccga.....cgcctcctaacattcacg 66

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents, NA:
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2: /cgn2_6/p10data/1/ina/5B.COMB.seq:*
3: /cgn2_6/p10data/1/ina/6A.COMB.seq:*
4: /cgn2_6/p10data/1/ina/6B.COMB.seq:*
5: /cgn2_6/p10data/1/ina/PCRUS.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24.2	36.7	2290	1	US-08-584-226-1
2	24.2	36.7	4403765	4	US-09-103-840A-2
3	22.4	33.9	3549	4	US-09-381-862-1
4	22.2	33.6	2700	1	US-08-484-106-5
5	22.2	33.6	2700	1	US-08-484-106-5
6	22.2	33.6	41676	3	US-09-356-952-12
7	22.2	33.3	1810	3	US-08-714-918-32
8	22.2	33.3	1810	4	US-09-265-315-32
9	22.2	33.3	1810	4	US-09-265-315-32
10	22.2	33.3	1810	4	US-09-266-417-32
11	21.6	33.0	2470	4	US-09-091-725-18
12	21.6	33.0	2546	4	US-09-091-725-12
13	21.8	32.7	730	1	US-07-826-945A-10
14	21.6	32.7	1065	2	US-08-444-646-5
15	21.6	32.7	1558	2	US-08-444-646-4
16	21.6	32.7	1558	2	US-08-444-646-4
17	21.2	32.1	4411529	4	US-09-103-840A-1
18	21.1	31.8	1380	2	US-08-748-947A-1
19	21.1	31.8	9432	2	US-08-277-231A-1
20	21.1	31.8	9432	2	US-08-473-750-4
21	21.1	31.8	9432	2	US-08-477-326-4
22	20.8	31.5	2504	1	US-08-484-105-15
23	20.8	31.5	2504	1	US-08-484-106-15
24	20.8	31.5	3980	1	US-08-233-008A-1
25	20.8	31.5	3980	1	US-08-233-008A-5
26	20.8	31.5	6519	1	US-08-233-008A-7
27	20.6	31.2	9100	2	US-08-743-637B-27

ALIGNMENTS

C 28	20.6	31.2	9100	3	US-08-526-840B-27	Sequence 27, Appl
C 29	20.4	30.9	230	3	US-08-532-896-28	Sequence 28, Appl
C 30	20.4	30.9	303	4	US-08-867-902F-2	Sequence 2, Appl
C 31	20.4	30.9	423	1	US-08-470-179-85	Sequence 85, Appl
C 32	20.4	30.9	472	2	US-08-465-380-33	Sequence 33, Appl
C 33	20.4	30.9	472	2	US-08-465-397-33	Sequence 33, Appl
C 34	20.4	30.9	472	2	US-08-466-396-33	Sequence 33, Appl
C 35	20.4	30.9	472	2	US-08-461-965-33	Sequence 33, Appl
C 36	20.4	30.9	472	2	US-08-634-641-33	Sequence 33, Appl
C 37	20.4	30.9	472	3	US-09-249-471-33	Sequence 33, Appl
C 38	20.4	30.9	472	3	US-09-249-472-33	Sequence 33, Appl
C 39	20.4	30.9	472	3	US-09-249-451-33	Sequence 33, Appl
C 40	20.4	30.9	472	3	US-08-609-455-33	Sequence 33, Appl
C 41	20.4	30.9	472	3	US-09-249-461-33	Sequence 33, Appl
C 42	20.4	30.9	472	3	US-09-249-448-33	Sequence 33, Appl
C 43	20.4	30.9	585	4	US-08-667-802F-3	Sequence 3, Appl
C 44	20.4	30.9	1407	3	US-08-668-988-7	Sequence 7, Appl
C 45	20.4	30.9	2156	4	US-08-965-762-18	Sequence 16, Appl

RESULT 1
US-08-584-226-1.
Sequence 1, Application US/08584226
Patent No. 5798240
GENERAL INFORMATION:
APPLICANT: Martinis, Susan A.
APPLICANT: Sassanfar, Mandana
APPLICANT: Kim, Sungheon
APPLICANT: Lee, Sang Ho
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL METHIONYL-tRNA
TITLE OF INVENTION: SYNTHETIC GENES, TESTER STRAINS AND ASSAYS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,226
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/305,766
FILING DATE: 13-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP194-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2290 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1563
US-08-584-226-1

Query Match 36.7% Score 24.2; DB 1; Length 2290;
Best Local Similarity 62.3%; Pred. No. 1.7;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

UY 6 TCTGATCTGCTTGCACAAACGGTAAACCGCTAGACTTACCGCTTACGAATTCAGCT 65
DB 1428 TCTGATCTGCTTGCACAAACGGTAAACCGCTAGACTTACCGCTTACGAATTCAGCT 1487

UY 66 G 66
DB 1488 G 1488

RESULT 2
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6274328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WITTE, Owen R.
APPLICANT: FRASER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24166-20007 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2
LENGTH: 440/4765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDS 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, c, g or g
US-09-103-840A-2

Query Match 36.7% Score 24.2; DB 4; Length 440/3765;
Best Local Similarity 62.3%; Pred. No. 9.4;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

UY 6 TCTGATCTGCTTGCACAAACGGTAAACCGCTAGACTTACCGCTTACGAATTCAGCT 65
DB 1125606 TCTGATCTGCTTGCACAAACGGTAAACCGCTAGACTTACCGCTTACGAATTCAGCT 1125547

UY 66 G 66
DB 1125546 G 1125546

RESULT 3
US-09-481-862-1
Sequence 1, Application US/09481862
Patent No. 6245906
GENERAL INFORMATION:
APPLICANT: Uyama, Hiroshi
APPLICANT: Abo, Kanako
APPLICANT: Koshi, Hiroyuki
APPLICANT: Matsui, Aki
TITLE OF INVENTION: PROBES FOR THE DIAGNOSIS OF INFECTIONS
TITLE OF INVENTION: CAUSED BY STREPTOCOCCUS PYOGENES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gotstein, Murray & Horan
STREET: 243 South Market Drive/6100 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/381,862
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1997-71077
FILING DATE: 25-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP98/01288
FILING DATE: 23-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Cawley, Jr., Thomas A.
REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 19036/36274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6400
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3549 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: Clinical Isolate Sp-6-28
US-09-381-862-1

Query Match 33.9% Score 22.4; DB 4; Length 3549;
Best Local Similarity 59.4%; Pred. No. 9.6;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

UY 1 TCGATCTGCATCGCTTGCACAAACGGTAAACCGCTAGACTTACCGCTTACGAATTCAGCT 60
DB 3046 TCGATCTGCATCGCTTGCACAAACGGTAAACCGCTAGACTTACCGCTTACGAATTCAGCT 3105

UY 61 GACG 64
DB 3106 TATC 3109

RESULT 4
US-08-484-105-5/c
Sequence 5, Application US/08484105
Patent No. 5589341
GENERAL INFORMATION:
APPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P.
APPLICANT: KOBAYASHI, Ryuji
APPLICANT: KINE, Jasper
APPLICANT: POSS, Margit
APPLICANT: McNALLY, Francis J.
APPLICANT: LAURENSEN, Patricia
APPLICANT: HERKOWITZ, Ira
APPLICANT: LI, Joachim J.
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALDRITTON & HERBERT
STREET: 4 Embarradero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
MOLECULE TYPE: CDNA
US-08-484-105-5

Query Match 33.6%; Score 22.2; DB 1; Length 2700;
Post Local Similarity 61.0%; Pred. No. 11;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0

QY 4 GAGTCGATCGTCGACCAACGGIAAAAAAGCGGTGATTACCGTCAGCAATCA 62
IDB 1586 GCGAGATATATTCACCAAAAGCATGTGAAAGATTACATTGCGATCAACCGATCA 1528

RESULT 5
US-08-484-106-5/c
Sequence 5, Application US/08484106
Patent No. 5614618
GENERAL INFORMATION:
APPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P
APPLICANT: KURAYASHI, Ryuji
APPLICANT: KINE, Jasper
APPLICANT: FOSS, Margit
APPLICANT: MCNALLY, Francis J
APPLICANT: LATHENSON, Patricia
APPLICANT: HERSHKOWITZ, Ira
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBACH, TEST, ALBERTSON & HERBERT
STREET: 4 Embarradero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299

```

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1      INFORMATION FOR SEQ ID NO: 5:
2      SEQUENCE CHARACTERISTICS:
3          LENGTH: 2700 base pairs
4          TYPE: nucleic acid
5          STRANDEDNESS: double
6          TOPOLOGY: linear
7      MOLECULE TYPE: cDNA
8      US-08-484-106-5
9
10     Query Match
11         Best Local Similarity 33.6%; Score 22.2; DB 1; Length 2700;
12         Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
13
14     QY 4 GATCGATCGGTCGACAAACGGGTAAAAAGCGGTAGATTACGGTCTAGCAATTC 62
15         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
16     Db 1586 GCTGAGCATGATTCACCAAAACGATCTGAAAAGATTAGTTGGCATCAACCGTATGCA 1528
17
18 RESULT 6
19 US-09-356-952-12/c
20 Sequence 12; Application US/09356952
21 Patent No. 6117663
22 GENERAL INFORMATION:
23 APPLICANT: Borjick-Sjodin, Ann
24 APPLICANT: Margaril, S. M.
25 APPLICANT: Bor-Sodi, Dafna
26 APPLICANT: Cole, Philip
27 APPLICANT: Kuriyan, John
28 TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
29 TITLE OF INVENTION: THEREOF
30 FILE REFERENCE: 600-1-228N
31 CURRENT APPLICATION NUMBER: US/09/356,952
32 CURRENT FILING DATE: 1999-07-19
33 EARLIER APPLICATION NUMBER: 60/093,631
34 EARLIER FILING DATE: 1998-07-21
35 NUMBER OF SEQ. ID NOS: 14
36 SOFTWARE: PatentIn Ver. 2.0
37 SEQ ID NO 12
38 LENGTH: 43676
39 TYPE: DNA
40 ORGANISM: Saccharomyces cerevisiae
41 US-09-356-952-12
42
43 Query Match
44         Best Local Similarity 33.6%; Score 22.2; DB 3; Length 43676;
45         Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
46
47     QY 4 GATCGATCGGTCGACAAACGGGTAAAAAGCGGTAGATTACGGTCTAGCAATTC 62
48         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
49     Db 30652 GCTGAGCATGATTCACCAAAACGATCTGAAAAGATTAGTTGGCATCAACCGTATGCA 30594
50
51 RESULT 7
52 US-08-714-918-32/c
53 Sequence 32; Application US/08714918
54 Patent No. 6037123
55 GENERAL INFORMATION:
56 APPLICANT: Benton, Bret
57 APPLICANT: Lee, Vinq
58 APPLICANT: Malouin, Francois
59 APPLICANT: Martin, Patrick K.
60 APPLICANT: Schmid, Molly B.
61 APPLICANT: Sun, Dongxu
62 TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTI-BACTERIAL
63 TITLE OF INVENTION: TARGET GENES
64 NUMBER OF SEQUENCES: 111
65 CORRESPONDENCE ADDRESS:
66 ADDRESSEE: Lyon & Lyon
67 STREET: 633 West Fifth Street
68 STREET: Suite 4700
69 CITY: Los Angeles
70 STATE: California
71 COUNTRY: U.S.A.

```

210: 00071 2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C., DOS 5.0
SOFTWARE: word perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/714-918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-1510
INFORMATION FOR SEQ. ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1810 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Matched 33.3% Score 227 DB 3 Length 1810;
Post Local Similarity 61.8%; Prod. No. 12;
Matches 34; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

CY 5 ATCTGATCTTCTCGCAAAACGGTAATAAAGCGGTACATTACGCTCTCAGCAT 59
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IDB 1669 ATCCGAATGCTTTTCATCAAAGAATAAACGAAGTAACGCTACCTGATACAT 1615

RESULT B
US 09 265 315-32/c
Sequence 32, Application US/09265315
Patent No. 6187541

GENERAL INFORMATION:
APPLICANT: Beionix, Inc.
APPLICANT: Lee, Wing J.
APPLICANT: Malinin, Francois
APPLICANT: Martin, Patrick R.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu

TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
ACTIVE ON STAPHYLOCOCCUS AUREUS

TITLE OF INVENTION: TARGET GENES

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C., DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO.: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1810 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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Query Match          33.48; Score 22; JB 4; Length 1810;
Best local Similarity 61.88; Pref. No. 12;
Matches 34; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

CY 5 ATTGATCGCTTCGACAAACCGTAAAGAGCGGTATTCGCTTCACAT 59
      ||||| ||||| || ||||| || ||||| || ||||| || ||
Db 1669 ATCGATCGCTTCCTTCACGAAAGGTAAAGCTAACGTTACGTCGATCAT 1615

RESULT 9
US-09-265-315-32/c
Sequence 32, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Beaton, Bret
APPLICANT: Lee, Vind J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Hongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STEPIERACXOUS ADREBS
NUMBER OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265, 315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714, 918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009, 102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003, 798
FILING DATE: September 15, 1995

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1  ATTORNEY/AGENT INFORMATION:
2  NAME: Warburg, Richard J.
3  REGISTRATION NUMBER: 32,327
4  REFERENCE/DOCKET NUMBER: 240/247
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: (213) 489-1600
7  TELEFAX: (213) 955-0440
8  TELFX: 67-3510
9  INFORMATION FOR SEQ ID NO: 32:
10 LENGTH: 1810 base pairs
11 TYPE: nucleic acid
12 STRANDBENESS: single
13 TOPOLOGY: linear
14
15 US-09-265-315-32
16
17 Query Match 33.3%; Score 22; DB 4; Length 1810;
18 Host Local Similarity 61.8%; Pred. No. 12;
19 Matches 34; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
20
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INFORMATION FOR SEQ ID NO.: 32:
SEQUENCE CHARACTERISTICS:
    LENGTH: 1810 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
US-09-266-417-32

Query Match          33.3%; Score 22; DB 4; Length 1810;
Best Local Similarity 61.8%; Pred. No. 12;
Matches   34; Conservative      0; Mismatches   21; Indels       0; Gaps        0;

QY     5 ATCTGATCGGTTCGCACAAAGCATAAAGGGTAGATTACCCTTACCAAI 59
      ||||| | | | | | | | | | | | | | | | | | | | | | |
Dd    1669 ATTGTGAATCCTTTTCACNNAAGAATAAAGAACGTACTGCCGTATCATI 1615


RESULT 11
Sequence 18, Application US/09091725
Patent No. 632914;
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Improved methods for transforming Pflaffia
TITLE OF INVENTOR: and recombinant DNA for use therein
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Morrison & Foerster LLP
STREET: 2000 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARES: PatentIn Release #1.0, Version #1.25 (RFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,725
FILING DATE: 23-DEC-1996
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: EP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: E. Victor Domagala
REGISTRATION NUMBER: 35,492
INFORMATION FOR SEQ ID NO.: 18:
SEQUENCE CHARACTERISTICS:
    LENGTH: 2470 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pfaffia rhodozyma
FEATURES:
    NAME/KEY: CDS
LOCATION: 177..2198
OTHER INFORMATION: /product= "Pcrfly"
US-09-091-725-18

Query Match          33.0%; Score 21.8; DB 4; Length 2470;
Best Local Similarity 61.4%; Pred. No. 15;
Matches   35; Conservative      0; Mismatches   22; Indels       0; Gaps         0;

QY     1 TGACATCTGATTCGTTCCACAANAAGCGTAATAAAGCGTAGATTACCGTGCCA 57
      || | | | | | | | | | | | | | | | | | | | | | | | |

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DB 2168 TGGATGTCGATCGGATCGCAAGGCGACTAGACACGGGAGAGGAGTATCGCAACACAA 2224

RESULT 12

US-09-091-725-12

Sequence 12, Application US/09091725

Patent No. 6329141

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Improved methods for transforming *Plattia*

TITLE OF INVENTION: and recombinant DNA for use therein

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

STREET: 2000 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: United States of America

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,725

FILING DATE: 23-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95201620.0

FILING DATE: 22-DEC-1995

APPLICATION NUMBER: EP 96200943.7

FILING DATE: 11-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: E. Victor Donahue

REGISTRATION NUMBER: 45,492

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 2546 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHEetical: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Plattia rhododyna*

FEATURE:

NAME/KEY: CDS

LOCATION: 225..2246

OTHER INFORMATION: /Product: "Prrt1B"

US-09-091-725-12

Query Match

Best Local Similarity 33.0%; Score 21.8; DB 4; Length 2546;

Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

DB 2216 TGGATGTCGATCGGATCGCAAGGCGACTAGACACGGGAGAGGAGTATCGCAACACAA 2272

US-09-091-725-22

RESULT 13

US-09-091-725-22

Sequence 22, Application US/09091725

Patent No. 6329141

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Improved methods for transforming *Plattia*

TITLE OF INVENTION: and recombinant DNA for use therein

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

STREET: 2000 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: United States of America

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,725

FILING DATE: 23-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95201620.0

FILING DATE: 22-DEC-1995

APPLICATION NUMBER: EP 96200943.7

FILING DATE: 11-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: E. Victor Donahue

REGISTRATION NUMBER: 45,492

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 3550 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHEtical: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Plattia rhododyna*

FEATURE:

NAME/KEY: CDS

LOCATION: 2293..3325

OTHER INFORMATION: /Product: "Prrt1B GR"

US-09-091-725-22

Query Match

Best Local Similarity 33.0%; Score 21.8; DB 4; Length 3550;

Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

DB 2216 TGGATGTCGATCGGATCGCAAGGCGACTAGACACGGGAGAGGAGTATCGCAACACAA 2272

US-09-091-725-22

RESULT 14

US-09-091-725-22

Sequence 22, Application US/09091725

Patent No. 6329141

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Improved methods for transforming *Plattia*

TITLE OF INVENTION: and recombinant DNA for use therein

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

STREET: 2000 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: United States of America

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,725

FILING DATE: 23-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95201620.0

FILING DATE: 22-DEC-1995

APPLICATION NUMBER: EP 96200943.7

FILING DATE: 11-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: E. Victor Donahue

REGISTRATION NUMBER: 45,492

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 3550 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA (genomic)

HYPOTHEtical: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Plattia rhododyna*

FEATURE:

NAME/KEY: CDS

LOCATION: 2293..3325

OTHER INFORMATION: /Product: "Prrt1B GR"

US-09-091-725-22

Query Match

Best Local Similarity 33.0%; Score 21.8; DB 4; Length 3550;

Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

DB 2216 TGGATGTCGATCGGATCGCAAGGCGACTAGACACGGGAGAGGAGTATCGCAACACAA 2272

US-09-091-725-22

RESULT 15

US-09-091-725-22

Sequence 22, Application US/09091725

Patent No. 6329141

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Improved methods for transforming *Plattia*

TITLE OF INVENTION: and recombinant DNA for use therein

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

STREET: 2000 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: United States of America

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,725

FILING DATE: 23-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95201620.0

FILING DATE: 22-DEC-1995

APPLICATION NUMBER: EP 96200943.7

FILING DATE: 11-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: E. Victor Donahue

REGISTRATION NUMBER: 45,492

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 3550 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA (genomic)

HYPOTHEtical: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: *Plattia rhododyna*

FEATURE:

NAME/KEY: CDS

LOCATION: 2293..3325

OTHER INFORMATION: /Product: "Prrt1B GR"

US-09-091-725-22

Query Match

Best Local Similarity 33.0%; Score 21.8; DB 4; Length 3550;

Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

DB 2216 TGGATGTCGATCGGATCGCAAGGCGACTAGACACGGGAGAGGAGTATCGCAACACAA 2272

US-09-091-725-22

Db 3295 TGTGTTATATAGCGGATGGGAAAGGCGAGTAAACACGCGGAGAAATACCGACACACAA 3351

RESULT 14

US-07-826-945A-10
Sequence 10, Application US/07826945A
Patent No. 5270179

GENERAL INFORMATION:

APPLICANT: Chatterjee, Deb K.

TITLE OF INVENTION: Cloning and Expression of 15 DNA

NUMBER OF SEQUENCES: 10
Polymerase Reduced In 3'-to-5' Exonuclease Activity

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue
CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/826,945A

FILING DATE: 19920128

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lewis, James L.

REGISTRATION NUMBER: 24,732

REFERENCE/DOCKET NUMBER: 0942,2270004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 466-0800

TELEFAX: (202) 834-8716

TELEX: 248636 SSR

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 730 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: Both

TOPOLOGY: Both

US-07-826-945A-10

Query Match: 32.7% Score 21.6; DB 1; Length 730;

Best Local Similarity: 63.5%; Pred. No. 14;

Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 530 CGTGTGAGAAATGCAAAAGTGTGATGATACCTCTACTACTACCCCTG 581

RESULT 15

US-08-444-646-5

Sequence 5, Application US/08444646

Patent No. 5837263

GENERAL INFORMATION:

APPLICANT: Hake, David A.

TITLE OF INVENTION: Leptospira MEMBRANE PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Flueton Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,646

FILING DATE: 19-MAY-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mong, Mean Khing

REGISTRATION NUMBER: 33,561

REFERENCE/DOCKET NUMBER: 5656-107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 977-1001

TELEFAX: (213) 977-1003

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1065 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-444-646-5

Query Match: 32.7% Score 21.6; DB 2; Length 1065;

Best Local Similarity: 75.0%; Pred. No. 15;

Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 594 AAGAGTAAAAAAGCGGTAGATTACCGTCTACGAA 58

594 AAGAGTAAAAAAGCGGTAGATTACCGTCTACGAA 629

Search completed: November 5, 2002, 06:19:06

Job time: 1892.3 secs

